

04684

From: Chan, Christina
Sent: Wednesday, April 17, 2002 3:51 PM
To: Yu, Misook; STIC-Biotech/ChemLib
Subject: RE: Rush search for 09/499,662

Please rush. Thanks Chris

-----Original Message-----

From: Yu, Misook
Sent: Wednesday, April 17, 2002 3:39 PM
To: Chan, Christina; STIC-Biotech/ChemLib
Subject: Rush search for 09/499,662

The case is due this bi-week. Would you please approve rush search for SEQID No:107 and 117? Thank you.

Examiner Misook Yu, Ph.D.
703-308-2454 (Phone)
Art Unit 1642
CM1-8E18 (Room)
CM1-8E12 (Mail Box)

RECEIVED
APR 17 2002
STIC

Point of Contact:
Barb O'Bryen
Technical Information Specialist
STIC CM1 6A05 308-4291

Searcher: MBP
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: 4-18-02
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST(where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 17, 2002, 16:36:27 ; Search time 40.38 Seconds
(without alignments)
436.588 Million cell updates/sec

Title: US-09-499-662-107

Perfect score: 1242

Sequence: 1 METDTILLVLLWPGSTG.....EVTHQGLSSPVTKSFNRGEC 238

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT.*
- 2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT.*
- 3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT.*
- 4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT.*
- 5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT.*
- 6: /SIDS8/gcgdata/geneseq/geneseq/AA1985.DAT.*
- 7: /SIDS8/gcgdata/geneseq/geneseq/AA1986.DAT.*
- 8: /SIDS8/gcgdata/geneseq/geneseq/AA1987.DAT.*
- 9: /SIDS8/gcgdata/geneseq/geneseq/AA1988.DAT.*
- 10: /SIDS8/gcgdata/geneseq/geneseq/AA1989.DAT.*
- 11: /SIDS8/gcgdata/geneseq/geneseq/AA1990.DAT.*
- 12: /SIDS8/gcgdata/geneseq/geneseq/AA1991.DAT.*
- 13: /SIDS8/gcgdata/geneseq/geneseq/AA1992.DAT.*
- 14: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT.*
- 15: /SIDS8/gcgdata/geneseq/geneseq/AA1994.DAT.*
- 16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT.*
- 17: /SIDS8/gcgdata/geneseq/geneseq/AA1996.DAT.*
- 18: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT.*
- 19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT.*
- 20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT.*
- 21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.*
- 22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1242	100.0	238	19 AAW83034	Anti-Fas humanised
2	1242	100.0	238	21 AAB14777	Humanised anti-Fas
3	1242	100.0	238	21 AAW90927	Humanised HFE7A de
4	1230	99.0	238	19 AAW83031	Anti-Fas humanised
5	1230	99.0	238	21 AAB14772	Humanised anti-Fas
6	1230	99.0	238	21 AAW90922	Humanised anti-Fas
7	1207	97.2	238	19 AAW83035	Anti-Fas humanised
8	1207	97.2	238	21 AAB14778	Humanised anti-Fas
9	1207	97.2	238	21 AAW90928	Humanised HFE7A de
10	1201	96.7	238	19 AAW83032	Anti-Fas humanised
11	1201	96.7	238	21 AAB14773	Humanised anti-Fas

12	1201	96.7	238	21 AAW90923	Humanised anti-Fas
13	1193	96.1	238	19 AAW83033	Anti-Fas humanised
14	1193	96.1	238	21 AAB14774	Humanised anti-Fas
15	1193	96.1	238	21 AAW90924	Humanised anti-Fas
16	1177	94.8	238	21 AAW90931	Humanised anti-Fas
17	1174	94.5	238	21 AAW90932	Humanised anti-Fas
18	1173	94.4	238	21 AAW90930	Humanised anti-Fas
19	1073.5	86.4	235	21 AAY93702	The kappa chain of
20	1073.5	86.4	235	21 AAY93729	The kappa chain of
21	1059	85.3	234	21 AAY93708	The kappa chain of
22	1059	85.3	234	21 AAY93733	The kappa chain of
23	1056.5	85.1	233	21 AAY93704	The kappa chain of
24	1056.5	85.1	233	21 AAY93731	The kappa chain of
25	1053	84.8	234	21 AAY92239	Human bone marrow-
26	1050	84.5	218	18 AAW13563	Humanised anti-L-s
27	1038.5	83.6	384	22 AAU14461	Human novel protei
28	1038.5	83.6	384	22 AAU14462	Human novel protei
29	1038.5	83.6	384	22 AAU14463	Human novel protei
30	1038.5	83.6	384	22 AAU14464	Human novel protei
31	1038	83.6	240	20 AAY50161	Human reshaped Flg
32	1036	83.4	218	20 AAW95658	Mus musculus anti-
33	1036	83.4	218	21 AAY85200	Light chain amino
34	1036	83.4	218	22 AAB76947	Full variable ligh
35	1035	83.3	236	22 AAG71272	Human gene 2-encod
36	1029	82.9	218	14 AAR33312	Humanised Maell ve
37	1017	81.9	237	20 AAW73873	Human antife epsll
38	1013	81.6	218	20 AAY50030	Human E27 anti-IgE
39	1013	81.6	218	20 AAW95660	Mus musculus anti-
40	1013	81.6	218	20 AAW95662	Mus musculus anti-
41	1013	81.6	218	21 AAB07472	Amino acid sequenc
42	1013	81.6	218	22 AAB74211	E27 anti-IgE antiB
43	1011	81.4	240	20 AAW73875	Human antife epsll
44	1010	81.3	218	20 AAW95669	Mus musculus anti-
45	1010	81.3	218	20 AAW95664	Mus musculus anti-

ALIGNMENTS

RESULT 1

AAW83034

ID AAW83034 standard; Protein; 238 AA.

XX

AC AAW83034;

XX

DT 15-MAR-1999 (first entry)

XX

DE Anti-Fas humanised antibody HFE7A light chain PDHH type.

XX

KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody; apoptosis; HFE7A; autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.

XX

OS Homo sapiens.

OS Synthetic.

XX

XX Key Location/Qualifiers

FT Peptide 1..20

FT Protein /label= Sig_peptide

FT Protein /label= Mat_protein

FT Region 21..131

FT Region /label= Variable

FT Region 132..238

FT Region /label= Constant

QY 1 METDTILLWVLLWVPGSTGEIVLTQSPGTLSLSPGERATLSCSKASQSDYDGDSDSYMMWY 60
 Db 1 metdtillwvllwvpgstgeivltqspgtlspsgeratlsckasqsgvdygdsgymwv 60
 QY 61 QOKQCAPRLIYAASNLESIGIPDRFSGSGCTDFTLTISRLEPDRFAVYTCQOSNEDPR 120
 Db 61 qkqpgqaprllyaaasnlesigipdrfsgsgctdftltisrlepdrfavytcqosnedpr 120
 QY 121 TFGQGTKEIKRTVAAPSVFIPPPSDEQLKSGTASVWCLLNFFYPREAKVQKVDNALQS 180
 Db 121 tfgggtkleikrtvaapsvfipppsdeqlksgtasvvcvllnffypreakvqkvdnalqs 180
 QY 161 GNSQESVTEQDSKSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTXSNRGE 238
 Db 161 gnsqesvteqdsksdyslsstltlskadyekhkyacevthqglsspvtksfnrgec 238

RESULT 3

AAW90927
 ID AAW90927 standard; Protein: 238 AA.

AC AAW90927;

XX
 DT 08-AUG-2000 (first entry)

XX
 DE Humanised HFE7A designed light chain protein.

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
 KW dermatological; immunosuppressive; thymimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjogren's syndrome; anemia; Addison's disease; sterility; myasthenia gravis;
 KW Goodpasture syndrome; Crohn's disease; scleroderma; gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX Synthetic.

XX EP990663-A2.

XX 05-APR-2000.

XX 29-SEP-1999; 99EP-0307711.

XX 30-SEP-1998; 98JP-0276881.

XX 30-SEP-1998; 98JP-0276882.

XX (SANY) SANKYO CO LTD.

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 PI WPI: 2000-258930/23.

XX N-PSDB: AAA11614.

XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems

XX Claim 3; Page 141-142; 263pp; English.

XX This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thymimetic,
 CC antirheumatic, nephrotropic, antinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiac and hepatropic activity. (I) induce

CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Sjogren's disease, rheumatoid arthritis, graft
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A designed light chain which is used in
 CC the method described in the invention.

XX Sequence 238 AA;

Query Match 100.0%; Score 1242; DB 21; Length 238;

Best Local Similarity 100.0%; Pred. No. 2.9e-68;

Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METDTILLWVLLWVPGSTGEIVLTQSPGTLSLSPGERATLSCSKASQSDYDGDSDSYMMWY 60

Db 1 metdtillwvllwvpgstgeivltqspgtlspsgeratlsckasqsgvdygdsgymwv 60

QY 61 QOKQCAPRLIYAASNLESIGIPDRFSGSGCTDFTLTISRLEPDRFAVYTCQOSNEDPR 120

Db 61 qkqpgqaprllyaaasnlesigipdrfsgsgctdftltisrlepdrfavytcqosnedpr 120

QY 121 TFGQGTKEIKRTVAAPSVFIPPPSDEQLKSGTASVWCLLNFFYPREAKVQKVDNALQS 180

Db 121 tfgggtkleikrtvaapsvfipppsdeqlksgtasvvcvllnffypreakvqkvdnalqs 180

QY 161 GNSQESVTEQDSKSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTXSNRGE 238

Db 161 gnsqesvteqdsksdyslsstltlskadyekhkyacevthqglsspvtksfnrgec 238

RESULT 4

AAW83031
 ID AAW83031 standard; Protein: 238 AA.

XX AC AAW83031;

XX 15-MAR-1999 (first entry)

XX Anti-Fas humanised antibody HFE7A light chain HH type.

XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

XX Peptide 1..20

XX Protein 21..238

XX /label= sig_peptide

XX /label= Mat_protein

FT Region 21..131
 /label= Variable
 FT Region 132..238
 /label= Constant
 FT Region 44..58
 /label= CDR_L1
 FT Region 74..80
 /note= "Claim 9"
 FT Region 74..80
 /label= CDR_L2
 FT Region 113..121
 /note= "claim 9"
 FT Region 113..121
 /label= CDR_L3
 FT Region 113..121
 /note= "Claim 9"
 PN AU9859701-A.
 PD 08-OCT-1998.
 XX 30-MAR-1998; 98AU-0059701.
 XX 08-OCT-1997; 97JP-0276064.
 PR 01-APR-1997; 97JP-0082953.
 PR 25-JUN-1997; 97JP-0169088.
 XX (SANY) SANKYO CO LTD.
 PA Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX WPI: 1998-543440/47.
 DR N-PSDB; AN70074.
 XX New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 XX Claim 21; Page 199-199; 292pp; English.
 PS This is the amino acid sequence of the HH type humanised light
 CC chain of murine anti-human Fas monoclonal antibody HFE7A.
 CC Humanisation of the murine sequence (see AAW83042) entailed making
 CC P47A, K49R, H80S, P81R, V82L, E84P, E85A, A87F and T89V amino acid
 CC substitutions; these residues are conserved in the human light
 CC chain (kappa chain). Host cell Escherichia coli PHSGHH7 SANK 73497
 CC harbors plasmid PHSGHH7 carrying a fusion fragment of the humanised
 CC HH type HFE7A light chain and DNA encoding the region of human
 CC immunoglobulin kappa chain, and is deposited as FERM BP-6073
 CC (claimed). The invention provides methods for producing humanised
 CC antibodies by culturing host cells. Humanised versions of HFE7A
 CC (see AAW83031-37), like native HFE7A, are capable of inducing
 CC apoptosis in abnormal cells expressing Fas, and of inhibiting
 CC Fas-induced apoptosis in normal cells. The humanised antibodies
 CC are used to evaluate, in animal models, treatments of diseases that
 CC involve Fas/Fas ligand interactions, and also to treat such
 CC diseases, including autoimmune disease (e.g. systemic lupus
 CC erythematosus, Hashimoto's disease, graft versus host disease,
 CC Sjogren syndrome, pernicious anaemia, Addison's disease,
 CC scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid
 CC arthritis, autoimmune haemolytic anaemia, sterility, myasthenia
 CC gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura
 CC and insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
 CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
 CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
 XX Sequence 238 AA;

Query Match 99.0%; Score 1230; DB 19; Length 238;
 Best Local Similarity 98.7%; Pred. No. 1.6e-67;
 Matches 235; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1.METDTILLWVPGSGEIVLTQSPGTLSLSPGERATLSCASQSDVDYDGDSTNNWY 60

Db 1 metdtillwvpgsgtdvltqspgtislsgeratlsckasqsdvdydgsynnwy 60
 QY 61 QOKPQAPRLIIYAASNLSEGIIDRFSGSGGTFTLTISRLEPEDFAVYYCQGSNEDPR 120
 Db 61 qokpqpaprliliyaasnlsgipdrfsgsggtfdtltisrlepafavyyccgsnedpr 120
 QY 121 TFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPRPAKVQWYDNALQS 180
 Db 121 tfgggttrleikrtvaapsvfifppsdeqlksgtasvvccllnnfyprpavkwvkdnlqs 180
 QY 181 GNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 238
 Db 181 gnsqesvteqdsksdystltskadyekhkvyacevthqglsspvtksfnrgec 238
 RESULT 5
 AAB14772
 ID AAB14772 standard; Protein; 238 AA.
 XX
 AC AAB14772;
 XX
 DT 24-NOV-2000 (first entry)
 XX
 DE Humanised anti-Fas antibody light chain, SEQ ID NO:50.
 XX
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
 KW murine; humanised antibody; complementarity determining region; CDR;
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
 KW hepatitis; AIDS; graft rejection; light chain.
 XX
 OS Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 XX
 PN JP2000169393-A.
 XX
 PD 20-JUN-2000.
 XX
 PF 30-SEP-1999; 99JP-0278301.
 XX
 PR 30-SEP-1998; 98JP-0276883.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 DR WPI: 2000-485645/43.
 DR N-PSDB; AAW72124.
 XX
 PT Preventive or treating agent for the diseases caused by an abnormality
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 PT anti-Fas antibody -
 XX
 PS Claim 20; Page 78-79; 139pp; Japanese.
 XX
 CC The invention relates to compositions for the prevention or treatment
 CC of diseases caused by an abnormality in the Fas/Fas ligand system
 CC containing an anti-Fas antibody as the active component. The anti-Fas
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 CC or a humanised version of HFE7A containing identical CDRs
 CC (complementarity determining regions) to antibody HFE7A. Via its
 CC interaction with Fas, the antibody of the invention acts as a modulator
 CC of apoptosis. The composition of the invention may therefore be used in
 CC the treatment or prevention of conditions such as autoimmune diseases,
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
 CC represent the light chains of several humanised HFE7A-derived anti-Fas
 CC antibodies.
 XX
 SQ Sequence 238 AA;

Query Match 99.0%; Score 1230; DB 21; Length 238;
 Best Local Similarity 98.7%; Pred. No. 1.6e-67;
 Matches 235; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 METDTILLWLLWVPGSTGEIVLTQSPGTLSPGERATLSCCKASQSDYDGSYMNWY 60
 DB 1 metdtillwllwvpgstgdvltqspgtlslspgeratlsckasqsdvdydgsymnw 60

QY 61 QORPGQAPRLIIYAASNLGSDIPDRFSGSGSGTDFTLTISRLEPEDFAVYCCQSNEDPR 120
 DB 61 qkpgqaprrlliyaasnlesgipdrfsgsgsgtdftltisrlepafavycqsgnedpr 120

QY 121 TFGOGTLEIKRTVAAPSVFPPSDEQLKSGTASVVCLLNNFYPRAKQVQKVDNALQS 180
 DB 121 tfgogtleikrtvaapsvfppsdqklsgtasvvcvllnnfypreakvqkvdnalqs 180

QY 181 GNSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 DB 181 gnsqesvteqdsksdystlslstltlskadyekhkvacevthqglsspvtksfnrgec 238

RESULT 6
 AAW90922 standard; Protein; 238 AA.

XX AC AAW90922;
 XX DT 08-AUG-2000 (first entry)
 XX DE Humanised anti-Fas antibody HFE7A light chain HH type protein.

XX KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; infertility; neuroprotective; antirheosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX OS Synthetic.
 XX PN EP90663-A2.
 XX PD 05-APR-2000.
 XX PE 29-SEP-1999; 99EP-0307711.
 XX PR 30-SEP-1998; 98JP-0276881.
 XX PR 30-SEP-1998; 98JP-0276882.
 XX PA (SANY) SANKYO CO LTD.
 XX PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 XX WP1: 2000-258930/23.
 XX DR N-PSDB; AAA11562.
 XX PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
 XX PT inflammatory or autoimmune disease, induces apoptosis selectively in
 XX PT cells with abnormal Fas-Fas ligand systems -
 XX PS Example reference 14; Page 114-115; 263pp; English.
 XX CC This invention describes a novel humanized anti-Fas antibody-like
 XX CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 XX CC ligand system, by binding to Fas on the cell surface, and prevents
 XX CC apoptosis in cells with a normal system, by inhibiting binding between
 XX CC Fas and its ligand. The products of the invention have anti-inflammatory,
 XX CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,

CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A light chain HH type which is used in
 CC the method described in the invention.
 XX
 SQ Sequence 238 AA;

Query Match 99.0%; Score 1230; DB 21; Length 238;
 Best Local Similarity 98.7%; Pred. No. 1.6e-67;
 Matches 235; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 METDTILLWLLWVPGSTGEIVLTQSPGTLSPGERATLSCCKASQSDYDGSYMNWY 60
 DB 1 metdtillwllwvpgstgdvltqspgtlslspgeratlsckasqsdvdydgsymnw 60

QY 61 QORPGQAPRLIIYAASNLGSDIPDRFSGSGSGTDFTLTISRLEPEDFAVYCCQSNEDPR 120
 DB 61 qkpgqaprrlliyaasnlesgipdrfsgsgsgtdftltisrlepafavycqsgnedpr 120

QY 121 TFGOGTLEIKRTVAAPSVFPPSDEQLKSGTASVVCLLNNFYPRAKQVQKVDNALQS 180
 DB 121 tfgogtleikrtvaapsvfppsdqklsgtasvvcvllnnfypreakvqkvdnalqs 180

QY 181 GNSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 DB 181 gnsqesvteqdsksdystlslstltlskadyekhkvacevthqglsspvtksfnrgec 238

RESULT 7
 AAW83035 standard; Protein; 238 AA.

XX AC AAW83035;
 XX DT 15-MAR-1999 (first entry)
 XX DE Anti-Fas humanised antibody HFE7A light chain PDHM type.

XX KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjorgen syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy.
 XX OS Homo sapiens.
 OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Peptide 1..20

FT Protein /label= Sig_peptide
 FT 21..238
 FT /label= Mat_protein
 FT 21..131
 FT /label= Variable
 FT 132..238
 FT /label= Constant
 FT 44..58
 FT /note= "claim 9"
 FT 74..80
 FT /label= CDR_L1
 FT /label= CDR_L2
 FT /note= "claim 9"
 FT 113..121
 FT /label= CDR_L3
 FT /note= "claim 9"
 XX AU9859701-A.
 XX
 PD 08-OCT-1998.
 XX
 PF 30-MAR-1998; 98AU-0059701.
 XX
 PR 08-OCT-1997; 97JP-0276064.
 PR 01-APR-1997; 97JP-0082953.
 PR 25-JUN-1997; 97JP-0169088.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 PI Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX
 DR WPI; 1998-543440/47.
 DR N-PSDB; AAV70078.
 XX
 PT New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 XX
 PS Claim 21; Page 220-221; 292pp; English.
 XX
 CC This is the amino acid sequence of the PDHM type humanised light
 CC chain of murine anti-human Fas monoclonal antibody HFE7A.
 CC Humanisation of the murine sequence (see AAW83042) entailed making
 CC DiE, P47A, K49R and R107K amino acid substitutions; these
 CC residues are conserved in the human light (kappa) chain. Host
 CC cell Escherichia coli pSHM2 SANK 70198 harbors plasmid pSHM2
 CC carrying a fusion of the humanised PDHM type HFE7A light chain and
 CC DNA encoding the region of human immunoglobulin kappa chain, and is
 CC deposited as FERM BP-6272 (claimed). The invention provides
 CC methods for producing humanised antibodies by culturing host
 CC cells. Humanised versions of HFE7A (see AAW83031-37), like native
 CC HFE7A, are capable of inducing apoptosis in abnormal cells
 CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal
 CC cells. The humanised antibodies are used to evaluate, in animal
 CC models, treatments of diseases that involve Fas/Fas ligand
 CC interactions, and also to treat such diseases, including autoimmune
 CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
 CC graft versus host disease, Sjogren syndrome, pernicious anaemia,
 CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
 CC sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,
 CC thrombopenia purpura and insulin-dependent diabetes), allergies,
 CC atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
 CC nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
 CC rejection (all claimed).
 XX
 SQ Sequence 238 AA;

Query Match 97.2%; Score 1207; DB 19; Length 238;
 Best Local Similarity 97.5%; Pred. No. 3.8e-66;

Matches 232; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 1 METDTILLWLLWVPGSTGEIVLTQSPGTLSLSPGERATLSCSKASQSYVDYDGDSYNNWY 60
 DB 1 metdtillwllwvpstgeivltqspgtlsispgeratlsckasqsvdydgdssymwy 60
 QY 61 QOKPGQAPRLIIYAASNLSEGIPIRFGSGSGTDFLTITSRLEPEDFAVYICQSQSNEDPR 120
 DB 61 qkpgqaprllyaaanlesgipdrfsgsgtdftitihpveedaatyycqsqnedpr 120
 QY 121 TFCQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRKAVQWKNALQS 180
 DB 121 tfcggtkleikrtvaapsvfifppsdeqlksgtasvvcillnmfypreakvqwkvdnals 180
 QY 181 GNSQESVTEQDSKDSYSLSTLTLSKADYKHKVACEVTHOGLSSPVTKSFNRGEC 238
 DB 181 gnsqesvteqdsksdyslsstltlskadyekhkvyacevthdgslspvcksnrgec 238
 RESULT 8
 AAB14778
 ID AAB14778 standard; Protein; 238 AA.
 XX
 AC AAB14778;
 XX
 DT 24-NOV-2000 (first entry)
 XX
 DE Humanised anti-Fas antibody light chain, SEQ ID NO:109.
 XX
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
 KW murine; humanised antibody; complementarity determining region; CDR;
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pannyelophthisis;
 KW hepatitis; AIDS; graft rejection; light chain.
 XX
 OS Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 XX
 PN JP2000169393-A.
 XX
 PD 20-JUN-2000.
 XX
 PF 30-SEP-1999; 99JP-0278301.
 XX
 PR 30-SEP-1998; 98JP-0276883.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 DR WPI; 2000-485645/43.
 DR N-PSDB; AAA72177.
 XX
 PT Preventive or treating agent for the diseases caused by an abnormality
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 PT anti-Fas antibody -
 XX
 PS Claim 20; Page 103; 139pp; Japanese.
 XX
 CC The invention relates to compositions for the prevention or treatment
 CC or diseases caused by an abnormality in the Fas/Fas ligand system
 CC containing an anti-Fas antibody as the active component. The anti-Fas
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 CC or a humanised version of HFE7A containing identical CDRs
 CC (complementarity determining regions) to antibody HFE7A. Via its
 CC interaction with Fas, the antibody of the invention acts as a modulator
 CC of apoptosis. The compositions of the invention may therefore be used in
 CC the treatment or prevention of conditions such as autoimmune diseases,
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
 CC represent the light chains of several humanised HFE7A-derived anti-Fas
 CC antibodies.
 XX

CC apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral, CC immunomodulatory, dermatological, immunosuppressive, thyromimetic, CC antirheumatic, nephrotropic, cardiatic, antiinfertility, neuroprotective, CC antiarteriosclerotic, cardiant and hepatotropic activity. (I) induce CC apoptosis by binding to cell surface Fas or inhibit it by competitive CC inhibition of ligand binding. (I) are used to treat and/or prevent CC diseases associated with the Fas/Fas ligand system, especially systemic CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively CC inhibit apoptosis in normal cells but selectively induce it in abnormal CC cells. They bind to both human and murine Fas, so can be evaluated in CC murine disease models. (I) act on the active site of Fas, i.e. they mimic CC the native ligand, do not induce liver disease, and have reduced risk of CC inducing a human anti-murine antibody response. This sequence represents CC a humanised anti-Fas antibody HFE7A designed light chain which is used in CC the method described in the invention.

XX
SQ Sequence 238 AA;

Query Match 97.2%; Score 1207; DB 21; Length 238;
Best Local Similarity 97.5%; Pred. No. 3.8e-66;
Matches 232; Conservative 1; Mismatches 5; Indels 0; Gaps

QY 1 METDTILLWLLVPGSGTGEIVLTQSPGTLSPGERATLSCASQSYVDYDGDSYMNY 60
Db 1 metdtillwllwpgstgeivltqspgtlslpgeratlscaksqsydygdSYMNY 60

QY 61 QOKPGQAPRLIIYAASNLSEGIPIRPSGSGTDFTLTISRLEPEDFAYYYCOOSNEDPR 120
Db 61 qokpgqaprllyaaanlesgipdrpsgsgtdftltihpveeadaatyccqgsnedpr 120

QY 121 TFGOGTKLEIKRTVAAPSVFIAPPDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQS 180
Db 121 tfgogtkleikrtvaapsvfippdeqlksgtasvcllnnfyreakvqwkvdnalqs 180

QY 181 GNSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 gnsqesvteqdsksdyslssltsltlskadyekhkvayacevthqglsspvtksfnrgec 238

RESULT 9
AAW90928
ID AAW90928 standard; Protein: 238 AA.
AC AAW90928;
XX 08-AUG-2000 (first entry)
XX Humanised HFE7A designed light chain protein #2.

DE DE
KW anti-body; human; anti-inflammatory; anti-anemic; antidiabetic;
KW dermatological; anti-arthritis; antiviral; immunomodulatory; cardiant;
KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
OS Synthetic.
XX EP990663-A2.
XX 05-APR-2000.
XX 29-SEP-1999; 99EP-0307711.
XX 30-SEP-1998; 98JP-0276881.
XX 30-SEP-1998; 98JP-0276882.
XX (SANY) SANKYO CO LTD.
XX
XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
XX WPI; 2000-258930/23.
XX N-PSDB; AAA11615.
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
XX inflammatory or autoimmune disease, induces apoptosis selectively in
XX cells with abnormal Fas-Fas ligand systems
XX Example reference 21; Page 144-145; 263pp; English.
XX
XX This invention describes a novel humanized anti-Fas antibody-like
XX molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
XX ligand system, by binding to Fas on the cell surface, and prevents
XX

XX FH Key Location/Qualifiers
 FT Peptide 1..20
 FT Protein /label= Sig_peptide
 FT Protein 21..238
 FT Region /label= Mat_protein
 FT Region 21..131
 FT Region /label= Variable
 FT Region 132..238
 FT Region /label= Constant
 FT Region 44..58
 FT Region /label= CDR_L1
 FT Region /note= "Claim 9"
 FT Region 74..80
 FT Region /label= CDR_L2
 FT Region /note= "Claim 9"
 FT Region 113..121
 FT Region /label= CDR_L3
 FT Region /note= "Claim 9"
 XX AU9859701-A.
 XX
 PD 08-OCT-1998.
 XX
 PF 30-MAR-1998; 98AU-0059701.
 XX
 PR 08-OCT-1997; 97JP-0276064.
 PR 01-APR-1997; 97JP-0082953.
 PR 25-JUN-1997; 97JP-0169088.
 XX
 XX (SANY) SANKYO CO LTD.
 XX
 PI Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX
 XX WPI: 1998-543440/47.
 DR N-PSDB; AA70075.
 DR
 DR
 DR
 XX New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 XX
 PS Claim 21; Page 200; 292pp; English.
 XX
 CC This is the amino acid sequence of the HM type humanised light
 CC chain of murine anti-human Fas monoclonal antibody HFE7A.
 CC Humanisation of the murine sequence (see AA83042) entailed making
 CC P47A and K49R amino acid substitutions; these residues are
 CC conserved in the human light (kappa) chain. Host cell E. coli
 CC PHSGHM17 SANK 73597 harbors plasmid PHSGHM17 carrying a fusion
 CC fragment of the humanised HM type HFE7A light chain and DNA
 CC encoding the region of human immunoglobulin kappa chain, and is
 CC deposited as FERM BP-6072 (claimed). The invention provides
 CC methods for producing humanised antibodies by culturing host
 CC cells. Humanised versions of HFE7A (see AA83031-37), like native
 CC HFE7A, are capable of inducing apoptosis in abnormal cells
 CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal
 CC cells. The humanised antibodies are used to evaluate, in animal
 CC models, treatments of diseases that involve Fas/Fas ligand
 CC interactions, and also to treat such diseases, including autoimmune
 CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
 CC graft versus host disease, Sjogren syndrome, pernicious anaemia,
 CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
 CC sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,
 CC thrombopenia purpura and insulin-dependent diabetes), allergies,
 CC atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
 CC nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
 CC rejection (all claimed).
 XX
 SQ Sequence 238 AA;

Query Match 96.7%; Score 1201; DB 19; Length 238;
 Best Local Similarity 96.6%; Pred. No. 8.9e-66;
 Matches 230; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 1 METDTILLWVLLWVPGSTGEIVLTQSPGTLSLSPGERATLSCAKASQSVYDGDSDYNNWY 60
 DB 1 metdtillwvllwvpgstgdvltqspgtlsispgeratlsckasqsvdygdsgymny 60
 QY 61 QOKPGOAPRLIIYAANLESGIPDRFSGSGTDFLTISRLEPEDFAVYVCOOSNEDPR 120
 DB 61 qkpggqaprllyaaanlesgipdrfsgsgtdftlthpveeedaatyycqgsnedpr 120
 QY 121 TFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRRAKYVQWYVDNALQS 180
 DB 121 tfgggtlrleikrtvaapsvfifppsdeqlksgtasvcllnnfyprreakyqwkvdnalqs 180
 QY 181 GNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSNRGE 238
 DB 181 gnsqesvteqdkdstyslslstltlskadyekkhvacevthgglaspvtcksfargec 238
 RESULT 11
 AABI4773
 ID AABI4773 standard; Protein; 238 AA.
 XX
 AC AABI4773;
 XX
 DT 24-NOV-2000 (first entry)
 XX
 DE Humanised anti-Fas antibody light chain, SEQ ID NO:52.
 XX
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
 KW murine; humanised antibody; complementarity determining region; CDR;
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pannyelophthisis;
 KW hepatitis; AIDS; graft rejection; light chain.
 XX
 OS Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 XX
 PN JP2000169393-A.
 XX
 PD 20-JUN-2000.
 XX
 PF 30-SEP-1999; 99JP-0278301.
 XX
 PR 30-SEP-1998; 98JP-0276883.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 DR WPI: 2000-485645/43.
 DR N-PSDB; AA72125.
 XX
 PT Preventive or treating agent for the diseases caused by an abnormality
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 PT anti-Fas antibody -
 XX
 PS Claim 20; Page 80-81; 139pp; Japanese.
 XX
 CC The invention relates to compositions for the prevention or treatment
 CC or diseases caused by an abnormality in the Fas/Fas ligand system
 CC containing an anti-Fas antibody as the active component. The anti-Fas
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 CC or a humanised version of HFE7A containing identical CDRs
 CC (complementarity determining regions) to antibody HFE7A. Via its
 CC interaction with Fas, the antibody of the invention acts as a modulator
 CC of apoptosis. The compositions of the invention may therefore be used in
 CC the treatment or prevention of conditions such as autoimmune diseases,
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 CC and organ graft rejection. Sequences AABI4772-BI4774 and AABI4777-BI4778

CC represent the light chains of several humanised HFE7A-derived anti-Fas
 CC antibodies.

XX Sequence 238 AA;

Query Match 96.7%; Score 1201; DB 21; Length 238;
 Best Local Similarity 96.6%; Pred. No. 8.9e-66;
 Matches 230; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 METDTILLWLLVPGSTGEIVLTQSPGTLSPGERATLSCASQSDYDGSYNNWY 60
 |||||
 Db 1 metdtillwllwpgstgdivltqspgtlslspgeratlsckasgsvdydgsymnw 60
 QY 61 QQRPGQAPRLIYAASNLGSGIDPRFSGSGGTDTLTISRLEPEDFAVYCYQOSNEDPR 120
 |||||
 Db 61 qkpgqgprilliyaasnlsgidprfsgsggtftltihpveedaatyccqgsnedpr 120
 QY 121 TFGOGTLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQS 180
 |||||
 Db 121 tfgogtltreikrtvaapsvfifppsdqksgtasvvccllnnfypreakvqwkvdnals 180
 QY 181 GNSQESVTEQDQSDYSTLSSTLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 |||||
 Db 181 gnsqesvteqdkdstylsstltlskadyekhkvacevthqglsspvtksfnrgec 238

RESULT 12

AAW90923

ID AAW90923 standard; Protein; 238 AA.

XX AAW90923;

XX 08-AUG-2000 (first entry)

XX Humanised anti-Fas antibody HFE7A light chain HM type protein.

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 XX anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 XX dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 XX nephrotropic; antinfertility; neuroprotective; antiartherosclerotic;
 XX hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 XX Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 XX Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 XX Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 XX multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 XX insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 XX cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

XX Synthetic.

XX EP990663-A2.

XX 05-APR-2000.

XX 29-SEP-1999; 99EP-0307711.

XX 30-SEP-1998; 98JP-0276881.

XX 30-SEP-1998; 98JP-0276882.

XX (SANY) SANKYO CO LTD.

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;

XX WPI; 2000-258930/23.

XX N-PSDB; AAA11563.

XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems
 XX Example reference 14; Page 117-118; 263pp; English.

CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antinfertility, neuroprotective,
 CC antiartherosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A light chain HM type which is used in
 CC the method described in the invention.

XX Sequence 238 AA;

Query Match 96.7%; Score 1201; DB 21; Length 238;
 Best Local Similarity 96.6%; Pred. No. 8.9e-66;
 Matches 230; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 METDTILLWLLVPGSTGEIVLTQSPGTLSPGERATLSCASQSDYDGSYNNWY 60
 |||||
 Db 1 metdtillwllwpgstgdivltqspgtlslspgeratlsckasgsvdydgsymnw 60
 QY 61 QQRPGQAPRLIYAASNLGSGIDPRFSGSGGTDTLTISRLEPEDFAVYCYQOSNEDPR 120
 |||||
 Db 61 qkpgqgprilliyaasnlsgidprfsgsggtftltihpveedaatyccqgsnedpr 120
 QY 121 TFGOGTLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQS 180
 |||||
 Db 121 tfgogtltreikrtvaapsvfifppsdqksgtasvvccllnnfypreakvqwkvdnals 180
 QY 181 GNSQESVTEQDQSDYSTLSSTLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 |||||
 Db 181 gnsqesvteqdkdstylsstltlskadyekhkvacevthqglsspvtksfnrgec 238

RESULT 13

AAW83033

ID AAW83033 standard; Protein; 238 AA.

XX AAW83033;

XX 15-MAR-1999 (first entry)

XX Anti-Fas humanised antibody HFE7A light chain MM type.

XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 XX apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjorgen syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy.

XX OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Peptide 1..20
FT /label= Sig_peptide
FT Protein 21..238
FT /label= Mat_protein
FT Region 21..131
FT /label= Variable
FT Region 132..238
FT /label= Constant
FT Region 44..58
FT /label= CDR_L1
FT /note= "claim 9"
FT Region 74..80
FT /label= CDR_L2
FT /note= "claim 9"
FT Region 113..121
FT /label= CDR_L3
FT /note= "claim 9"
XX AU9859701-A.
XX
XX 08-OCT-1998.
XX
XX 30-MAR-1998; 98AU-0059701.
XX
XX 08-OCT-1997; 97JP-0276064.
XX 01-APR-1997; 97JP-0082953.
XX 25-JUN-1997; 97JP-0169088.
XX
XX (SANY) SANKYO CO LTD.
XX
XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
XX Masahiko O, Nobufusa S, Shin Y, Tohru T;
XX
XX WPI; 1998-543440/47.
XX N-PSDB; AAV70076.
XX
XX New antibodies and proteins bind conserved epitope of Fas antigen -
XX used to evaluate drugs in animal models and to treat Fas-associated
XX diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
XX myocarditis, hepatitis and AIDS
XX
XX Claim 21: Page 202; 292pp; English.
XX
XX This is the amino acid sequence of the MM type humanised light
XX chain of murine anti-human Fas monoclonal antibody HFE7A. E. coli
XX SANK 73697 harbors plasmid pHSMM6 carrying a fusion fragment of the
XX humanised MM type HFE7A light chain and DNA encoding the region of
XX human kappa chain, and is deposited as FERM BP-6071 (claimed). The
XX invention provides methods for producing humanised antibodies by
XX culturing host cells. Humanised versions of HFE7A (see AAW83031-37),
XX like native HFE7A, are capable of inducing apoptosis in abnormal
XX cells expressing Fas, and of inhibiting Fas-induced apoptosis in
XX normal cells. The humanised antibodies are used to evaluate, in
XX animal models, treatments of diseases that involve Fas/Fas ligand
XX interactions, and also to treat such diseases, including autoimmune
XX disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
XX graft versus host disease, Sjogren syndrome, pernicious anaemia,
XX Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
XX disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
XX sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,
XX thrombopenia purpura and insulin-dependent diabetes), allergies,
XX atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
XX nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
XX rejection (all claimed).
XX
XX Sequence 238 AA;

Query Match 96.1%; Score 1193; DB 19; Length 238;
Best Local Similarity 95.8%; Pred. No. 2.7e-65;
Matches 228; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 1 METDTILLWVLLWVPGSTGEIVLTQSPGTLSLSPGERATLSCSKASQSVYDGDSDYMNWY 60
Db 1 metdtillwvllwvpgstgdvltqspgtlsispgeratlsckasqsvdydgdsmwy 60
QY 61 QQRPGQAPRLIYAANLESIGIPDRFSGSGGTDFLTITISRLPEDFAVYVCOQSNEDPR 120
Db 61 qqkpgqppklliyaanlesigipdrfsgsggtldftlthpveedaatyycqgsnedpr 120
QY 121 TFCQGTKLEIKRTVAAPSVFIFPPSDQKLSGTASVVCVLLNNFYPREAKYQWKVDNALQS 180
Db 121 tfcggtrleikrtvaapsvfifppsdqklsgtasvvcvllnnfypreakyqwkvdnalqs 180
QY 181 GNSQESVTEQDSKDSYSLSTLTLSKADYKHKVACEVTHQGLSSPVTKSNRGEC 238
Db 181 gnsqesvteqdsksdyslsstltlskadyekhkvacevthqglsspvtksnrgec 238
RESULT 14
AAB14774
ID AAB14774 standard; Protein; 238 AA.
XX AC AAB14774;
XX
XX 24-NOV-2000 (first entry)
XX
XX Humanised anti-Fas antibody light chain, SEQ ID NO:54.
XX
XX Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
XX murine; humanised antibody; complementarity determining region; CDR;
XX human Fas; Fas ligand; apoptosis modulator; programmed cell death;
XX autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
XX cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
XX hepatitis; AIDS; graft rejection; light chain.
XX
XX Chimeric - Mus musculus.
XX Chimeric - Homo sapiens.
XX
XX JP2000169393-A.
XX
XX 20-JUN-2000.
XX
XX 30-SEP-1999; 99JP-0278301.
XX
XX 30-SEP-1998; 98JP-0276883.
XX
XX (SANY) SANKYO CO LTD.
XX
XX WPI; 2000-485645/43.
XX N-PSDB; AAA72126.
XX
XX Preventive or treating agent for the diseases caused by an abnormality
XX in the Fas/Fas ligand system e.g. autoimmune diseases, contains
XX anti-Fas antibody
XX
XX Claim 20; Page 83; 139pp; Japanese.
XX
XX The invention relates to compositions for the prevention or treatment
XX or diseases caused by an abnormality in the Fas/Fas ligand system
XX containing an anti-Fas antibody as the active component. The anti-Fas
XX antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
XX or a humanised version of HFE7A containing identical CDRs
XX (complementarity determining regions) to antibody HFE7A. Via its
XX interaction with Fas, the antibody of the invention acts as a modulator
XX of apoptosis. The composition of the invention may therefore be used in
XX the treatment or prevention of conditions such as autoimmune diseases,
XX allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
XX glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
XX and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
XX represent the light chains of several humanised HFE7A-derived anti-Fas

CC antibodies.
XX Sequence 238 AA;
SQ

Query Match 96.1%; Score 1193; DB 21; Length 238;
Best Local Similarity 95.8%; Pred. No. 2.7e-65;
Matches 228; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 METDTILLWLLVPGSTGEIVLTQSPGTLSLSPGERATLSCSKASQSVYDGDSDSYMMWY 60
DB 1 metdtillwllwvpgstgdivltqspgtlsispggeratlsckasqsvdydgdsmw 60

QY 61 QOKPQAPRLIIYAASNLESGIPDRFSGSGTDFTLTISRLEPEDFAVYCCQSNEDPR 120
DB 61 qokpqprrlliiyaasnlesgipdrfsgsgtdftltihpveeadaatyccqsnedpr 120

QY 121 TFGGOTKLEIKRTVAAPSVFIAPPSSQSLKSGTASVVCLLNFPREAKVQWKVDNALQS 180
DB 121 tfgggtrleikrtvaapsvfifppssdeqlksgtasvvcllnfnpreakvqwkvdnalqs 180

QY 181 GNSQESVTEQDSKDSYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
DB 181 gnsqesvteqdsksdystlsstltlskadyekhkvyacevthqglsspvtksfnrgec 238

RESULT 15
AAW90924
ID AAW90924 standard; Protein: 238 AA.
AC AAW90924;
XX
DT 08-AUG-2000 (first entry)
XX

Humanised anti-Fas antibody HFE7A light chain MM type protein.
XX
KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW nephrotropic; antifertility; neuroprotective; antitumor; sclerotic;
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX
OS Synthetic.
XX
XX EP990663-A2.
XX
XX 05-APR-2000.
XX
XX 29-SEP-1999; 99EP-0307711.
XX
XX 30-SEP-1998; 98JP-0276881.
XX
XX 30-SEP-1998; 98JP-0276882.
XX
XX (SANY) SANKYO CO LTD.
XX
XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
XX
XX WPI; 2000-258930/23.
XX
XX N-PSDB; AAA11564.
XX
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
XX inflammatory or autoimmune disease, induces apoptosis selectively in
XX cells with abnormal Fas-Fas ligand systems
XX
XX Example reference 14; Page 119-120; 263pp; English.
XX
XX This invention describes a novel humanized anti-Fas antibody-like

Search completed: April 17, 2002, 16:38:53
Job time: 146 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 17, 2002, 16:36:57 ; Search time 21.24 Seconds
(without alignments)
252.156 Million cell updates/sec

Title: US-09-499-662-107
Perfect score: 1242
Sequence: 1 METDILLWVLLWPGSTG.....EVTHOGLSPVTKSFNRGEC 238

Scoring table: BLOSUMP62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1050	84.5	218	5	PCT-US96-13152-2
2	1036	83.4	218	2	US-08-887-352B-13
3	1036	83.4	218	3	US-08-466-151-9
4	1036	83.4	218	4	US-09-109-207C-13
5	1036	83.4	218	4	US-09-296-005-13
6	1013	81.6	218	4	US-09-282-505-1
7	1013	81.6	218	4	US-09-054-255-1
8	1010	81.3	218	2	US-08-887-352B-15
9	1010	81.3	218	2	US-08-887-352B-17
10	1010	81.3	218	2	US-08-887-352B-19
11	1010	81.3	218	2	US-08-887-352B-24
12	1010	81.3	218	4	US-09-109-207C-15
13	1010	81.3	218	4	US-09-109-207C-17
14	1010	81.3	218	4	US-09-109-207C-19
15	1010	81.3	218	4	US-09-109-207C-24
16	1010	81.3	218	4	US-09-296-005-15
17	1010	81.3	218	4	US-09-296-005-17
18	1010	81.3	218	4	US-09-296-005-19
19	1010	81.3	218	4	US-09-296-005-24
20	979.5	78.9	241	2	US-07-916-098A-56
21	976.5	78.6	239	3	US-08-487-550-6
22	976	78.6	234	4	US-09-049-672A-6
23	966.5	77.8	235	1	US-08-276-852-153
24	966.5	77.8	235	1	US-08-899-575-153
25	966.5	77.8	235	1	US-08-899-575-153
26	966.5	77.8	235	1	PCT-US95-08743-153
27	958.5	77.2	233	2	US-07-934-373C-25

28 958.5 77.2 233 3 US-08-437-642B-25
29 958.5 77.2 233 5 PCT-US93-07832-25
30 957.5 77.1 235 4 US-09-171-945-97
31 956.5 77.0 214 2 US-08-480-753-6
32 956.5 77.0 214 3 US-09-041-889-11
33 956.5 77.0 214 3 US-08-837-058-11
34 955 76.9 214 3 US-07-934-373C-39
35 955 76.9 214 3 US-08-437-642B-39
36 955 76.9 214 5 PCT-US93-07832-39
37 955 76.9 236 1 US-08-157-101A-5
38 950 76.5 214 2 US-07-934-373C-40
39 950 76.5 214 2 US-08-788-800-11
40 950 76.5 214 3 US-08-437-642B-40
41 950 76.5 214 3 US-09-097-309-2
42 950 76.5 214 4 US-09-097-171A-2
43 950 76.5 214 5 PCT-US93-07832-40
44 950 76.5 237 3 US-09-097-309-6
45 950 76.5 237 4 US-09-097-171A-10

ALIGNMENTS

RESULT 1
PCT-US96-13152-2
; Sequence 2, Application PC/TUS9613152
; GENERAL INFORMATION:
; APPLICANT: Martin, Ulrich, et al.
; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ f
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; ADDRESSEE: Attn: Norman D. Hanson
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Computer Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13152
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/578,953
; FILING DATE: 27-Dec-95
; APPLICATION NUMBER: EP 95 112 895.8
; FILING DATE: 17-Aug-95
; APPLICATION NUMBER: EP 95 114 969.9
; FILING DATE: 19-Sep-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Norman D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-13152-2

Query Match 84.5%; Score 1050; DB 5; Length 218;
Best Local Similarity 91.3%; Pred. NO. 2a-81;

QY 141 IFPPSDEQLKSGTASVYVCLLNFFPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 200
 Db 121 IFPPSDEQLKSGTASVYVCLLNFFPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180

QY 201 STLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 Db 181 STLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 4
 US-09-109-207C-13
 ; Sequence 13, Application US/09109207C
 ; Patent No. 6172213
 ; GENERAL INFORMATION:
 ; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
 ; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
 ; FILE REFERENCE: P1123R1
 ; CURRENT APPLICATION NUMBER: US/09/109,207C
 ; CURRENT FILING DATE: 1998-06-30
 ; PRIOR APPLICATION NUMBER: US 60/051,554
 ; PRIOR FILING DATE: 1997-07-03
 ; NUMBER OF SEQ ID NOS: 44
 ; SEQ ID NO 13
 ; LENGTH: 218
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; NAME/KEY: Artificial
 ; LOCATION: 1-218
 ; OTHER INFORMATION: Light chain sequence derived from MAE11
 US-09-109-207C-13

Query Match 83.4%; Score 1036; DB 4; Length 218;
 Best Local Similarity 89.9%; Pred. No. 3.1e-80;
 Matches 196; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 21 EIVLTQSPGTLSPGERATLSCASQSDYDGDSDYNNWYQOKPGQAPRLIIYAASNLES 80
 Db 1 DIQLTQSPSSLSASVGDRTITCRASQSDYDGDSDYNNWYQOKPGKAPKLLIYAASYLE 60
 QY 81 GIPDRFSGSGGTDFLTITISRLPEDEFAVYCCQSNEDPRTFGQGTKEIKRTVAAPSVF 140
 Db 61 GVPDRFSGSGGTDFLTITISRLPEDEFAVYCCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
 QY 141 IFPPSDEQLKSGTASVYVCLLNFFPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 200
 Db 121 IFPPSDEQLKSGTASVYVCLLNFFPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
 QY 201 STLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 Db 181 STLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 5
 US-09-296-005-13
 ; Sequence 13, Application US/09296005
 ; Patent No. 6290957
 ; GENERAL INFORMATION:
 ; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
 ; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
 ; FILE REFERENCE: P1123C1r
 ; CURRENT APPLICATION NUMBER: US/09/296,005
 ; CURRENT FILING DATE: 1999-04-21
 ; EARLIER APPLICATION NUMBER: US 08/887,352
 ; EARLIER FILING DATE: 1997-07-02
 ; NUMBER OF SEQ ID NOS: 26
 ; SEQ ID NO 13
 ; LENGTH: 218
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; NAME/KEY: Artificial

; LOCATION: 1-218
 ; OTHER INFORMATION: Light chain sequence derived from MAE11
 US-09-296-005-13

Query Match 83.4%; Score 1036; DB 4; Length 218;
 Best Local Similarity 89.9%; Pred. No. 3.1e-80;
 Matches 196; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 21 EIVLTQSPGTLSPGERATLSCASQSDYDGDSDYNNWYQOKPGQAPRLIIYAASNLES 80
 Db 1 DIQLTQSPSSLSASVGDRTITCRASQSDYDGDSDYNNWYQOKPGKAPKLLIYAASYLE 60
 QY 81 GIPDRFSGSGGTDFLTITISRLPEDEFAVYCCQSNEDPRTFGQGTKEIKRTVAAPSVF 140
 Db 61 GVPDRFSGSGGTDFLTITISRLPEDEFAVYCCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
 QY 141 IFPPSDEQLKSGTASVYVCLLNFFPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 200
 Db 121 IFPPSDEQLKSGTASVYVCLLNFFPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
 QY 201 STLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 Db 181 STLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 6
 US-09-282-505-1
 ; Sequence 1, Application US/09282505A
 ; Patent No. 6194551
 ; GENERAL INFORMATION:
 ; APPLICANT: Esche Ekinaduese Idusogie et al.
 ; TITLE OF INVENTION: Polypeptide Variants
 ; FILE REFERENCE: P1266R1
 ; CURRENT APPLICATION NUMBER: US/09/282,505A
 ; CURRENT FILING DATE: 1999-03-31
 ; NUMBER OF SEQ ID NOS: 2
 ; SEQ ID NO 1
 ; LENGTH: 218
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; NAME/KEY: Artificial Sequence
 ; LOCATION: 1-218
 ; OTHER INFORMATION: Sequence is completely synthesized
 ; Patent No. 6194551
 US-09-282-505-1

Query Match 81.6%; Score 1013; DB 4; Length 218;
 Best Local Similarity 88.1%; Pred. No. 2.7e-78;
 Matches 192; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

QY 21 EIVLTQSPGTLSPGERATLSCASQSDYDGDSDYNNWYQOKPGQAPRLIIYAASNLES 80
 Db 1 DIQLTQSPSSLSASVGDRTITCRASKPVDGEGSDYNNWYQOKPGKAPKLLIYAASYLE 60
 QY 81 GIPDRFSGSGGTDFLTITISRLPEDEFAVYCCQSNEDPRTFGQGTKEIKRTVAAPSVF 140
 Db 61 GVPDRFSGSGGTDFLTITISRLPEDEFAVYCCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
 QY 141 IFPPSDEQLKSGTASVYVCLLNFFPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 200
 Db 121 IFPPSDEQLKSGTASVYVCLLNFFPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
 QY 201 STLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 Db 181 STLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 7
 US-09-054-255-1
 ; Sequence 1, Application US/09054255


```
QY 81 GIPDRFSGSGTDFLTISRLEPEDFAVYCCQSNEDPRTFGQGTKEIKRTVAAPSVF 140
Db 61 GVPSRFSGSGGTDFLTISRLEPEDFAVYCCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
QY 141 IFPPSDEQLKGTASVWCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 200
Db 121 IFPPSDEQLKGTASVWCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180
QY 201 STLTLSKADYKHKYACAEVTHQGLSSPVTKSFNRGEC 238
Db 181 STLTLSKADYKHKYACAEVTHQGLSSPVTKSFNRGEC 218

RESULT 10
US-08-887-352B-19
; Sequence 19, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-19

Query Match 81.3%; Score 1010; DB 2; Length 218;
Best Local Similarity 87.6%; Pred. No. 4.8e-78;
Matches 191; Conservative 15; Mismatches 12; Indels 0; Gaps 0;

QY 21 EIVLTQSPGTLISLSPGERATLSCAKSQSYVDYDGSYMNWYQOKPGQAPRLIIYAASNL 80
Db 1 DIQLTQSPSSLASVSGDRVITCRASKPVDGSDSYLNWYQOKPGKAPKLLIIYAASYLE 60
QY 81 GIPDRFSGSGTDFLTISRLEPEDFAVYCCQSNEDPRTFGQGTKEIKRTVAAPSVF 140
Db 61 GVPSRFSGSGGTDFLTISRLEPEDFAVYCCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
QY 141 IFPPSDEQLKGTASVWCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 200
Db 121 IFPPSDEQLKGTASVWCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180
QY 201 STLTLSKADYKHKYACAEVTHQGLSSPVTKSFNRGEC 238
Db 181 STLTLSKADYKHKYACAEVTHQGLSSPVTKSFNRGEC 218

RESULT 12
US-09-109-207C-15
; Sequence 15, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
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RESULT 11
US-08-887-352B-24
; Sequence 24, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-24

Query Match 81.3%; Score 1010; DB 2; Length 218;
Best Local Similarity 87.6%; Pred. No. 4.8e-78;
Matches 191; Conservative 15; Mismatches 12; Indels 0; Gaps 0;

QY 21 EIVLTQSPGTLISLSPGERATLSCAKSQSYVDYDGSYMNWYQOKPGQAPRLIIYAASNL 80
Db 1 DIQLTQSPSSLASVSGDRVITCRASKPVDGSDSYLNWYQOKPGKAPKLLIIYAASYLE 60
QY 81 GIPDRFSGSGTDFLTISRLEPEDFAVYCCQSNEDPRTFGQGTKEIKRTVAAPSVF 140
Db 61 GVPSRFSGSGGTDFLTISRLEPEDFAVYCCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
QY 141 IFPPSDEQLKGTASVWCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 200
Db 121 IFPPSDEQLKGTASVWCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180
QY 201 STLTLSKADYKHKYACAEVTHQGLSSPVTKSFNRGEC 238
Db 181 STLTLSKADYKHKYACAEVTHQGLSSPVTKSFNRGEC 218

RESULT 12
US-09-109-207C-15
; Sequence 15, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
```


US-09-109-207C-24

Query Match		81.3%;	Score 1010;	DB 4;	Length 218;
Best Local Similarity		87.6%;	Pred. No. 4.8e-78;		
Matches 191;		Conservative 15;	Mismatches 12;	Indels 0;	Gaps 0;

Qy	21	EIVLTQSPGTLSPGERATLSC	KASQSDYDGD	SYMNWYQOKPG	QAPRLLIYAAS	NLES 80
Db	1	DIQLTQSPFSSLSASVGD	RVTITCRASKPVD	GEDSYLNWYQOKPG	KAPKLLIYAAS	YLES 60
Qy	81	GIPDRFSGSGGTDFLT	ISRLPEDP	AVYYCQOSNEDP	RTFGG	TKLEIKRTVAAPSVF 140
Db	61	GVPFRFSGSGGTDFLT	ISLQPEDF	ATYYCQOSHEDP	YTFGG	TKVEIKRTVAAPSVF 120
Qy	141	IFPPSDEQLKSGTASV	VVCLLN	NFYPREAKVQ	KVDNALQSGNSQ	ESVTEQDSKDS
Db	121	IFPPSDEQLKSGTASV	VVCLLN	NFYPREAKVQ	KVDNALQSGNSQ	ESVTEQDSKDS
Qy	201	STLTLSKADYEKHKV	YACEVTHQGL	SSPVT	KSFNRGEC	238
Db	181	STLTLSKADYEKHKV	YACEVTHQGL	SSPVT	KSFNRGEC	218

Search completed: April 17, 2002, 16:39:21
Job time: 144 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 17, 2002, 16:37:07 ; Search time 25.85 Seconds
(without alignments)
701.336 Million cell updates/sec

Title: US-09-499-662-107
Perfect score: 1242
Sequence: 1 METDFTLLWVLLWVPGSNG.....EVTHQGLSSPVTKSFNRGEC 238

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	996.5	80.2	215	2 JE0242	Ig kappa chain NIG
2	950.5	76.5	215	2 JE0244	Ig kappa chain NIG
3	941.5	75.8	215	2 A23746	Ig kappa chain V-I
4	927.5	74.7	215	2 JE0243	Ig kappa chain NIG
5	884	71.2	216	2 JE0241	Ig kappa chain Am3
6	801	64.5	240	2 S06084	Ig kappa chain pre
7	749	60.3	218	2 S68241	Ig kappa chain V r
8	743	59.8	218	2 JC5810	monoclonal antibod
9	723	58.2	220	2 A31790	Ig kappa chain V r
10	722	58.1	234	2 S14237	Ig kappa chain pre
11	720.5	58.0	219	2 PC4203	Ig kappa chain (mo
12	720.5	58.0	219	2 S38865	Ig kappa chain - m
13	714.5	57.5	219	2 S52028	Ig kappa chain - m
14	714	57.5	210	2 A56169	Ig kappa chain V r
15	712.5	57.4	225	2 S37484	Ig kappa chain - m
16	711.5	57.3	230	2 S33161	Ig kappa chain - s
17	708.5	57.0	217	2 S42772	Ig kappa chain - m
18	699.5	56.3	235	2 S25058	Ig kappa chain - m
19	698.5	56.2	219	2 S16112	Ig kappa chain V r
20	692	55.7	234	2 S01320	Ig kappa chain pre
21	690.5	55.6	225	2 JL0029	Ig kappa chain pre
22	687	55.3	214	2 S68212	Ig kappa chain (Ma
23	622	50.1	178	2 PT0219	Ig kappa chain V-C
24	614.5	49.5	197	2 S29593	Ig kappa chain (WM
25	605.5	48.8	135	2 S52059	JC-kappa protein -
26	583	46.9	144	2 PL0106	Ig kappa chain pre
27	582.5	46.9	239	2 A20969	Ig kappa chain pre
28	576	46.4	131	2 PH1226	Ig kappa chain pre
29	564.5	45.5	145	2 S20631	Ig kappa chain - n

30	563.5	45.4	238	2 A49633	Ig lambda-like cha
31	548	44.1	106	1 K3HU	Ig kappa chain C r
32	541.5	43.6	129	1 K3HUHA	Ig kappa chain pre
33	539.5	43.4	128	2 S20636	Ig kappa chain V r
34	536.5	43.2	129	2 S49532	anti-5m antibody V
35	528.5	42.6	129	1 K3HUHI	Ig kappa chain pre
36	528	42.5	131	1 KVM5M6	Ig kappa chain pre
37	525.5	42.3	129	2 S46369	Ig light chain var
38	525.5	42.3	134	2 S38643	Ig kappa chain V r
39	516.5	41.6	129	2 A32274	Ig kappa chain pre
40	513	41.3	99	2 A37927	Ig kappa chain C r
41	511	41.1	128	2 A56701	Ig kappa chain V r
42	510	41.1	132	1 KVM532	Ig kappa chain pre
43	508	40.9	233	2 S29577	Ig light chain - r
44	507	40.8	99	2 S26653	Ig kappa chain C r
45	505.5	40.7	130	2 S20637	Ig kappa chain V r

ALIGNMENTS

RESULT 1
JE0242
Ig kappa chain NIG26 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0242
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda
submitted to JIPID, November 1998
A:Description: Structure relationship of kappatype light chains with AL amyloidosis:
A:Reference number: JE0241
A:Accession: JE0242
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 80.2%; Score 996.5; DB 2; Length 215;
Best Local Similarity 89.4%; Pred. No. 1.7e-57;
Matches 195; Conservative 8; Mismatches 12; Indels 3; Gaps 1;

Qy	21	EIVLTQSPGTLSPGERATLSCAKASQSDVDGDSVMYQKPGQAPRLIIYAASNLES	80
Db	1	EIVLTQSPGTLSPGERATLSCASQSV---SNNYLAWYQKPGQAPSLIIYDASSRAT	57
Qy	81	GIPDRFSGSGGTFTLTISRLEPEDFAVYYCQQSNEDPRTFGQGTKEIKRTVAAPSVF	140
Db	58	GIPDRFSGSGGTFTLTISRLEPEDFAVYYCQQYDRPPTFGQGTKEIKRTVAAPSVF	117
Qy	141	IFPPSDEQLKSGTASVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLS	200
Db	118	IFPPSDEQLKSGTASVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLS	177
Qy	201	STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC	238
Db	178	STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC	215

RESULT 2
JE0244
Ig kappa chain NIG2 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0244
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.
submitted to JIPID, November 1998
A:Description: A new subgroup of k type light chains (VkV) identified in cases of AL
A:Reference number: JE0243
A:Accession: JE0244
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology

F;16-90/Domain: immunoglobulin homology <IMM>

Query Match	76.5%	Score 950.5	DB 2	Length 215
Best Local Similarity	86.3%	Pred. No. 1.5e-54		
Matches 189	Conservative	8	Mismatches 17	Indels 5
				Gaps 2

Qy	21	EIVLTQSPGTLISLSPGERATLVCSKASQSDVYDGDSTNNYVQKPGQAPRLIIYAASNLIS	80
Db	1	EWLTQSPATLVSPGERATLVCSRASQV---HSLNLAIVQKPGQAPRLIIYRASTRAT	56
Qy	81	GIPDRFGSGSGDTFTLTISRLEPDEFAVYYCOOSNE-DRPTFGQCTKLEIKRTVAAPSV	139
Db	57	GIPARFSGSGSGDTFTLTISLQSEDFALYICQYINWPPLTFGGGTVKEIKRTVAAPSV	116
Qy	140	FIFPPSDEQLKSGTASVVCVLNNFYPREAKVQMKVDNALQSGNSQESVTEQDSKDSYSL	199
Db	117	FIFPPSDEQLKSGTASVVCVLNNFYPREAKVQMKVDNALQSGNSQESVTEQDSKDSYSL	176
Qy	200	SSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC	238
Db	177	SSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC	215

RESULT 3
A23746
Ig kappa chain v-III (KAU cold agglutinin) - human
C;Species: Homo sapiens (man)
C;date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C;Accession: A23746

F; Leonl, J.; Ghiso, J.; Gohl, F.; Frangione, B.
 J. Biol. Chem. 286, 2835-2842, 1991
 A: Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglobulin
 A: Reference number: A23746; MUID: 91131575
 A: Accession: A23746
 A: Status: preliminary
 A: Molecule type: protein
 A: Residues: 1-215 <LEO>
 C: Superfamily: immunoglobulin v region; immunoglobulin homology
 C: Keywords: heterotetramer; immunoglobulin
 F: 16-91/Domain: immunoglobulin homology <IMM>

Query Match	75.8%;	Score 941.5;	DB 2;	Length 215;
Best Local Similarity	88.0%;	Pred. NO. 5.7e-54;		
Matches 191;	Conservative	5;	Mismatches 18;	Indels 3;
				Gaps 1;

[illegible]

RESULT 4
JE0243
Ig kappa chain NIG93 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0243
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T
submitted to JIPID, November 1998
A:Description: A new subgroup of k type light chains (Vk) identified in cases of AL amy

A;Reference number: JE0243
A;Accession: JE0243
A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobu
F;16-90/Domain: immunoglob

Query Match	74.7%;	Score 927.5;	DB 2;	Length 215;
Best Local Similarity	84.0%;	Pred. NO. 4.5e-53;		
Matches 184;	Conservative 12;	Mismatches 18;	Indels 5;	Gaps 2;

Qy	21	EIVTQSPGTLTSLSPGERATLSCKASQSVYDGDGSYNNWYQQPQAPRLLIYAANLSE 80
		: : : : : : : : : : : 81
Db	1	EIVNTQSPATLSVSPGERATLSCRASQSV-----ATNVVWYMQKLGQAPRLLIYDASTRAT 56
Qy	81	GIPDFSGSGSGTDFTLTISRLEPDEFAVYVCOQSNEDPRTFGQGTKEIK-RTVAAPSV 139
Db		: : : : : : : : : : 140
	57	GVPAKFSGSGSGTEFTLTISLQSEDAFYIYQHNNAWPPTFGQGTKEIKRTVAAPSV 116
Qy	140	FIFPPSDEQLKSGTASVYVCLLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSTYSYL 199
Db		: : : : : : : : : : 198
	117	FIFPPSDEQLKSGTASVYVCLLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSTYSYL 176
Qy	200	SSTLTSLKADYEKKHYACEVTHQGLSSPVTYKSFNRGEC 238
Db		: : : : : : : : : : 239
	177	SSTLTSLKADYEKKHYACEVTHQGLSSPVTYKSFNRGEC 215

```

RESULT      5
JE0241
Ig kappa chain Am37 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0241
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda
submitted to JIPID, November 1998
A:Description: Structure relationship of kappa type light chains with AL amyloidosis:
A:Reference number: JE0241
A:Accession: JE0241
A:Molecule type: protein
A:Residues: 1-216 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-92/Domain: immunoglobulin homology <IMM>

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Query Match 71.2%; Score 884; DB 2; Length 216;
Best Local Similarity 80.3%; Pred. No. 2.8e-50;
Matches 175; Conservative 17; Mismatches 24; Indels 2; Gaps 2;

Qy	21	EIVLTQSPGTLISLSPGERATLSCAKASQSVVDYDGDSTNYWYQQKPGQAPRLIIYAASNLGS	80
Db	1	DIIVTQSPDFLAYSLSGERATINCKSQSVLYSKNFLAWYQQKPGQ-PKLLIIW-ANVRFS	58
Qy	81	GIPDRFGSGSGGDFTLTISRLEPEDFAVYVCOGSNEDPRTGCGNKLEIKRTVAAPSVF	140
Db	59	GVDPDRFGSGVGDFTLTISNLQAEILVAVYVCOQYSTYPSFGQGRLEIKRTVAAPSVF	118
Qy	141	IFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS	200
Db	119	IFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS	178
Qy	201	STLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC	238
Db	179	STLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC	216

```

RESULT      6
S06084
Ig kappa chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C;Accession: S06084

```


R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.

Nucleic Acids Res. 17, 7992, 1989

A:Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA

A:Reference number: S06084; MUID:9001688

A:Accession: S06084

A:Molecule type: mRNA

A:Residues: 1-240 <CRO>

A:Cross-references: EMBL:X16129; NID:956457; PIDN:CAA34256.1; PID:956458

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-240/Product: Ig kappa chain #status predicted <MAT>

F:153-222/Domain: immunoglobulin homology <IMM>

Query Match 64.5%; Score 801; DB 2; Length 240;
Best Local Similarity 62.5%; Pred. No. 6.8e-45;
Matches 150; Conservative 37; Mismatches 51; Indels 2; Gaps 1;

QY 1 METDTILLWLLVWPGTCEIVLTQSPGTLSPGERATLSCSKASQSDYDGD--SYMN 58

Db 1 MESQTQVLSLLWISGTGDFVMTQSPSSLAIVSAGETVITNCKSSQSLFYSGNQKNYLA 60

QY 59 WYQKPGQAPRLIYAASNLGSDIPRFGSGSGTFTLTISRLEPEDEFAVYVCOQSNED 118

Db 61 WYQKPGQSKLLIYWASTRQSGVDPDRFIGSGSGTFTLTISRVAQEDLAIYVCLQYET 120

QY 119 PRTEGQGTLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNAL 178

Db 121 PYTFGAGTKLELRADAAPTIFPPSTEQALATGGASVVCCLNNFYPRDISVKKIDGTE 180

QY 179 QSGNSQSVTEQDSKDSYSLSSLTLSKADYEKKHYVACEVTHQGLSSPVTKSFNRGEC 238

Db 181 RRGVLDVSDTDQDSKDSYSLSSLTLSKADYESHNLTYCEVHKTSSPVVVKSFNRNEC 240

RESULT 7

S68241

Ig kappa chain V region (Mab13-1) - mouse (fragment)

N:Alternate names: immunoglobulin light chain

C:Species: Mus musculus (house mouse)

C:Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000

C:Accession: S68241; S68214

R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.

submitted to the EMBL Data Library, March 1994

A:Description: Specific peroxidase activity by formation of an antibody L-chain-porphyrin

A:Reference number: S68241

A:Accession: S68241

A:Molecule type: mRNA

A:Residues: 1-218 <TAK>

A:Cross-references: EMBL:D29670; NID:9473962; PIDN:BA06141.1; PID:9473963

R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.

FEBS Lett. 375, 273-276, 1995

A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin

A:Reference number: S68211; MUID:96085223

A:Accession: S68214

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 'N1', 3-212 <TAW>

A:Cross-references: EMBL:D29670

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

Query Match 60.3%; Score 749; DB 2; Length 218;
Best Local Similarity 64.7%; Pred. No. 1.4e-41;
Matches 141; Conservative 29; Mismatches 48; Indels 0; Gaps 0;

QY 21 EIVLTQSPGTLSPGERATLSCSKASQSDYDGSYMNWYQKPGQAPRLIYAASNLDES 80

Db 1 ELVLTQSPASLAVSLGQRATISCRASKSVASGYIYHMYQKPGQPKLLISLATNLES 60

QY 81 GIPDRFGSGSGTFTLTISRLEPEDEFAVYVCOQSNEDPRTFGGQTKLEIKRTVAAPSVF 140

Best Local Similarity 60.9%; Pred. No. 6.5e-40;
Matches 134; Conservative 35; Mismatches 49; Indels 2; Gaps 1;

Db 61 GVPARFSGSGGTFTLTISRLEPEDEFAVYVCOHNSRELPLTFGAGTKLELRADAAPTYS 120

QY 141 IFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSKDSYSLS 200

Db 121 IFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSKDSYSLS 180

QY 201 STLTLSKADYEKKHYVACEVTHQGLSSPVTKSFNRGEC 238

Db 181 STLTLSKADYEKKHYVACEVTHQGLSSPVTKSFNRGEC 218

RESULT 8

JC5810

monoclonal antibody 13-1 light chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000

C:Accession: JC5810

R:Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, T.

Biochem. Biophys. Res. Commun. 240, 566-572, 1997

A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porp

A:Reference number: JC5810; MUID:98063277

A:Accession: JC5810

A:Molecule type: protein

A:Residues: 1-218 <AKA>

C:Comment: This catalytic antibody has peroxidase oxidase. It is directed against a p

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 59.8%; Score 743; DB 2; Length 218;

Best Local Similarity 65.0%; Pred. No. 3.3e-41;

Matches 141; Conservative 27; Mismatches 49; Indels 0; Gaps 0;

QY 22 IVLTQSPGTLSPGERATLSCSKASQSDYDGSYMNWYQKPGQAPRLIYAASNLDES 81

Db 2 IVLTQSPASLAVSLGQRATISCRASKSVASGYIYHMYQKPGQPKLLISLATNLES 61

QY 82 IPDRFSGSGGTFTLTISRLEPEDEFAVYVCOQSNEDPRTFGGQTKLEIKRTVAAPSVFI 141

Db 62 VPARFSGSGGTFTLTISRLEPEDEFAVYVCOHNSRELPLTFGAGTKLELRADAAPTYSI 121

QY 142 FPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSKDSYSLSS 201

Db 122 FPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSKDSYSLSS 181

QY 202 TLTLTKADYEKKHYVACEVTHQGLSSPVTKSFNRGEC 238

Db 182 TLTLTKADYEKKHYVACEVTHQGLSSPVTKSFNRGEC 218

RESULT 9

A31790

Ig kappa chain V region (17/9) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000

C:Accession: A31790

R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.

J. Biol. Chem. 263, 17100-17105, 1988

A:Title: Preliminary crystallographic data, primary sequence, and binding data for an

A:Reference number: A92686; MUID:89034213

A:Accession: A31790

A:Molecule type: mRNA

A:Residues: 1-220 <SCH>

A:Cross-references: GB:M23626; GB:J04061; NID:9533234; PIDN:AAA39162.1; PID:9533235

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 58.2%; Score 723; DB 2; Length 220;

Best Local Similarity 60.9%; Pred. No. 6.5e-40;

Matches 134; Conservative 35; Mismatches 49; Indels 2; Gaps 1;

RESULT 15
S37484
Ig kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
C:Accession: S37484
R:Duccancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A:Reference number: S37483
A:Accession: S37484
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-225 <DUC>
A:Cross-references: EMBL:X70424; NTD:g406254; PIDN:CAA49869.1; PID:g406255
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

[illegible]

Search completed: April 17, 2002, 16:39:53
Job time: 166 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 17, 2002, 16:38:12 ; Search time 17.09 Seconds
(without alignments)
510.604 Million cell updates/sec

Title: US-09-499-662-107

Perfect score: 1242

Sequence: 1 METDILLWVLLWVPGSTG.....EVTHQGLSPVTKSPNRGEC 238

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	548	44.1	106	1 KAC_HUMAN	P01834 homo sapien
2	541.5	43.6	129	1 KV3L_HUMAN	P18135 homo sapien
3	538.5	42.6	129	1 KV3M_HUMAN	P18136 homo sapien
4	528	42.5	131	1 KV3I_MOUSE	P01661 mus musculus
5	510	41.1	132	1 KV3F_MOUSE	P01658 mus musculus
6	494	39.8	128	1 KV3K_HUMAN	P06311 homo sapien
7	478	38.5	111	1 KV3M_MOUSE	P01665 mus musculus
8	476	38.3	111	1 KV3N_MOUSE	P01666 mus musculus
9	474	38.2	111	1 KV3O_MOUSE	P01667 mus musculus
10	471	37.9	111	1 KV3Q_MOUSE	P01669 mus musculus
11	469.5	37.8	109	1 KV3B_HUMAN	P01620 homo sapien
12	468.5	37.7	109	1 KV3D_HUMAN	P01622 homo sapien
13	468.5	37.7	129	1 KV3H_HUMAN	P04207 homo sapien
14	464.5	37.4	109	1 KV3E_HUMAN	P01623 homo sapien
15	463	37.3	111	1 KV3L_MOUSE	P01664 mus musculus
16	455	36.6	115	1 KV3I_HUMAN	P04433 homo sapien
17	453.5	36.5	110	1 KV3P_MOUSE	P01668 mus musculus
18	447.5	36.0	109	1 KV3G_HUMAN	P04206 homo sapien
19	442	35.6	134	1 KV4C_HUMAN	P06314 homo sapien
20	436.5	35.1	108	1 KV3A_HUMAN	P01619 homo sapien
21	433.5	34.9	133	1 KV2F_HUMAN	P01664 mus musculus
22	431	34.7	111	1 KV3H_MOUSE	P06310 homo sapien
23	429.5	34.6	116	1 KV3J_HUMAN	P01660 mus musculus
24	426.5	34.3	133	1 KV4B_HUMAN	P04434 homo sapien
25	423	34.1	111	1 KV3J_MOUSE	P06313 homo sapien
26	422	34.0	111	1 KV3K_MOUSE	P01662 mus musculus
27	422	34.0	129	1 KV1W_HUMAN	P01663 mus musculus
28	415	33.4	111	1 KV3R_MOUSE	P04431 homo sapien
29	411.5	33.1	109	1 KV3F_HUMAN	P01670 mus musculus
30	409.5	33.0	100	1 KV3C_HUMAN	P01624 homo sapien
31	408	32.9	114	1 KV4A_HUMAN	P01621 homo sapien
32	407	32.8	111	1 KV3S_MOUSE	P01625 homo sapien
33	406	32.7	111	1 KV3U_MOUSE	P01671 mus musculus
					P01673 mus musculus

34	404	32.5	112	1 KV3G_MOUSE	P01659 mus musculus
35	401	32.3	108	1 KAC_HUMAN	P01603 homo sapien
36	401	32.3	111	1 KV3T_MOUSE	P01672 mus musculus
37	400	32.2	108	1 KV1H_HUMAN	P01600 homo sapien
38	400	32.2	111	1 KV3C_MOUSE	P01656 mus musculus
39	397	32.0	111	1 KV3A_MOUSE	P01654 mus musculus
40	395	31.8	108	1 KV1M_HUMAN	P01605 homo sapien
41	394	31.7	108	1 KV1M_HUMAN	P01606 homo sapien
42	393.5	31.7	117	1 KV2E_HUMAN	P06309 homo sapien
43	391	31.5	108	1 KV1G_HUMAN	P01599 homo sapien
44	390.5	31.4	113	1 KV2D_HUMAN	P01617 homo sapien
45	389.5	31.4	112	1 KV3B_MOUSE	P01655 mus musculus

ALIGNMENTS

RESULT 1					
KAC_HUMAN					
ID	KAC_HUMAN	STANDARD;	PRT;	106 AA.	
AC	P01834;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	20-AUG-2001 (Rel. 40, Last annotation update)				
DE	IG KAPPA CHAIN C REGION.				
GN	IGKC.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE (MYELOMA PROTEIN EU).				
RX	MEDLINE=71064023; PubMed=5489770;				
RA	Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;				
RT	"The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain."				
RT	Biochemistry 9:3155-3161(1970).				
RL	[2]				
RP	DISULFIDE BONDS.				
RX	MEDLINE=71064027; PubMed=4923144;				
RA	Gall W.E., Edelman G.M.;				
RT	"The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds."				
RL	Biochemistry 9:3188-3196(1970).				
RN	[3]				
RP	SEQUENCE (BENCE-JONES PROTEIN TI).				
RX	MEDLINE=72188439; PubMed=5027703;				
RA	Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;				
RT	"Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein TI). IV. The complete amino acid sequence and its significance for the mechanism of antibody production."				
RT	Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=81042304; PubMed=6775818;				
RA	Hietter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;				
RT	"Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments."				
RL	Cell 22:197-207(1980).				
RN	[5]				
RP	SEQUENCE (BENCE-JONES PROTEIN ROY).				
RA	Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.;				
RA	(In) Franek F., Shugar D. (eds.);				
RL	Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).				
RN	[6]				
RP	SEQUENCE (BENCE-JONES PROTEIN CUM).				
RX	MEDLINE=68242259; PubMed=5586923;				
RA	Hilschmann N.;				
RT	"The complete amino acid sequence of Bence Jones protein Cum (kappa-type)."				

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RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [7]
RP SEQUENCE (BENCE-JONES PROTEIN AG).
RX MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges.";
RL J. Biol. Chem. 244:3350-3360(1969).
RN [8]
RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains.";
RL Science 169:56-59(1970).
CC -!- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
CC 45-ALA & 83-VAR. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC
CC MARKER, 45-ALA AND 83-LEU.
CC -----
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CC -----
DR EMBL; J00241; AAA58989.1; -
DR EMBL; V00557; CAA23823.1; -
DR PIR; A02116; K3HU.
DR MIM; 147200;
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; Igc1; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 26 86
FT DISULFID 106 106
FT VARIANT 83 83
FT INTERCHAIN (WITH A HEAVY CHAIN).
FT V -> L (IN INV(1,2) MARKER).
FT /FTIG=VAR_003897.
FT D -> N (IN REF. 7 AND 8).
FT E -> Q (IN REF. 5 AND 6).
FT CONFLICT 14 14
FT CONFLICT 57 57
FT SEQUENCE 106 AA; 11609 MW; 5198401FDD372CE8 CRC64;
SQ

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Query Match 44.1%; Score 548; DB 1; Length 106;
 Best Local Similarity 100.0%; Pred. No. 1.6e-38; Mismatches 0; Indels 0; Gaps 0;
 Matches 106; Conservative 0;

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QY 133 TVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 192
Db 1 TVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60
QY 193 KSTYSLSTLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 61 KSTYSLSTLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 106

```

RESULT 2

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ID KV3M_HUMAN STANDARD; PRT; 129 AA.
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION HAH PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
CC PIR; PL0022; K3HUHA.
DR HSSP; P01789; 2MCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igc; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 56 70 FRAMEWORK 2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 78 109 FRAMEWORK 3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
FT SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;
SQ

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Query Match 43.6%; Score 541.5; DB 1; Length 129;
 Best Local Similarity 80.3%; Pred. No. 6.9e-38;
 Matches 106; Conservative 9; Mismatches 14; Indels 3; Gaps 1;

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QY 1 METDITLLWVLLWPGSTGEIVLTQSPGTLSLSPGERATLSCASQSVDDYDGSINWY 60
Db 1 METPAQLLFLLWLEPDTTGEIVLTQSPGTLSLSPGERATLSCASQSV---SSYLAWY 57
QY 61 QKPGQAPRLIYAASNLSESGDTPDFSGSGSDFTLTISRLEPEDFVAVYCOOSNEDPR 120
Db 58 QKPGQAPRLIYGASSRATGIPDFSGSGSDFTLTISRLEPEDFVAVYCOQYGTSPR 117
QY 121 TFGQGTKEIKR 132
Db 118 TFGQGTKEIKR 129

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RESULT 3

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ID KV3M_HUMAN STANDARD; PRT; 129 AA.
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION HIC PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
CC PIR; PL0021; K3HUHI.
DR HSSP; P01789; 2MCP.

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RESULT 8
KV3N_MOUSE
ID KV3N_MOUSE STANDARD; PRT; 111 AA.
AC P01667;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7183.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity."
RL Nature 276:785-790(1978).
DR PIR; B01937; KVM583.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;

Query Match 38.38; Score 476; DB 1; Length 111;
Best Local Similarity 81.1%; Pred. No. 1.3e-32;
Matches 90; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 21 EIVLTQSPGTLSPGERATLSCASQSDVDGDSYMNWYQKPGQAPRLLIYAASNL 80
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYMNWYQKPGQAPRLLIYAASNL 60

Qy 81 GIPDRFSGSGTDFTLNISRLPEDEFAVYCCQSNEDPRTFGQGTKLEIK 131
Db 61 GIPARFSGSGTDFTLNIHPVEEDAATYCCQSNEDPLTFGAGTKLEIK 111

RESULT 9
KV3Q_MOUSE
ID KV3Q_MOUSE STANDARD; PRT; 111 AA.
AC P01667;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 6308.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity."
RL Nature 276:785-790(1978).
DR PIR; C01937; KVM508.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.

Query Match 38.38; Score 476; DB 1; Length 111;
Best Local Similarity 81.1%; Pred. No. 1.3e-32;
Matches 90; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 21 EIVLTQSPGTLSPGERATLSCASQSDVDGDSYMNWYQKPGQAPRLLIYAASNL 80
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYMNWYQKPGQAPRLLIYAASNL 60

Qy 81 GIPDRFSGSGTDFTLNISRLPEDEFAVYCCQSNEDPRTFGQGTKLEIK 131
Db 61 GIPARFSGSGTDFTLNIHPVEEDAATYCCQSNEDPLTFGAGTKLEIK 111

RESULT 9
KV3Q_MOUSE
ID KV3Q_MOUSE STANDARD; PRT; 111 AA.
AC P01667;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 6308.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity."
RL Nature 276:785-790(1978).
DR PIR; C01937; KVM508.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
```

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DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match 38.2%; Score 474; DB 1; Length 111;
Best Local Similarity 81.1%; Pred. No. 2e-32;
Matches 90; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

Qy 21 EIVLTQSPGTLSPGERATLSCASQSDVDGDSYMNWYQKPGQAPRLLIYAASNL 80
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYMNWYQKPGQAPRLLIYAASNL 60

Qy 81 GIPDRFSGSGTDFTLNISRLPEDEFAVYCCQSNEDPRTFGQGTKLEIK 131
Db 61 GIPARFSGSGTDFTLNIHPVEEDAATYCCQSNEDPRTFGQGTKLEIK 111

RESULT 10
KV3Q_MOUSE
ID KV3Q_MOUSE STANDARD; PRT; 111 AA.
AC P01669;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7769.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity."
RL Nature 276:785-790(1978).
DR PIR; E01937; KVM569.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;

Query Match 37.9%; Score 471; DB 1; Length 111;
Best Local Similarity 80.2%; Pred. No. 3.5e-32;
Matches 89; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

Qy 21 EIVLTQSPGTLSPGERATLSCASQSDVDGDSYMNWYQKPGQAPRLLIYAASNL 80
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYMNWYQKPGQAPRLLIYAASNL 60
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QY 81 GIPDRFSGSGGDTFTLTISRLEPEDFAVYCYQSQNSNEDPRTFGGKLEIK 131
DB 61 GIPARFSGSGGDTFTLTNIHPVEEDAATYCYQSQNSNEDPRTFGGKLEIK 111

RESULT 11
KV3D_HUMAN
ID KV3D_HUMAN STANDARD; PRT; 109 AA.
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION SIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human Igm anti-gamma-globulins of the Wa
RT group."
RL Biochemistry 20:5816-5822(1981).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR; A01892; K3HUSI.
DR HSP; P01789; 2MCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89
FT NON_TER 109 109
FT BY SIMILARITY.
SQ SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;

Query Match 37.8%; Score 469.5; DB 1; Length 109;
Best Local Similarity 81.2%; Pred. No. 4.5e-32;
Matches 91; Conservative 9; Mismatches 9; Indels 3; Gaps 1;

QY 21 EIVLTQSPGTLSPGERATLSCASQSVYDGDSDYNNWYQKPGQAPRLIYAASNLES 80
DB 1 EIVLTQSPGTLSPGERATLSCASQSVYDGDSDYNNWYQKPGQAPRLIYAASNLES 80
QY 81 GIPDRFSGSGGDTFTLTISRLEPEDFAVYCYQSQNSNEDPRTFGGKLEIKR 132
DB 58 GIPDRFSGSGGDTFTLTISRLEPEDFAVYCYQSQNSNEDPRTFGGKLEIKR 109

RESULT 12
KV3D_HUMAN
ID KV3D_HUMAN STANDARD; PRT; 109 AA.
AC P01622;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION TI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72188439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT ti). IV. The complete amino acid sequence and its significance for
RT the mechanism of antibody production."
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
```

```
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01895; K3HUTI.
DR HSP; P01789; 2MCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 23 89
FT NON_TER 109 109
FT BY SIMILARITY.
SQ SEQUENCE 109 AA; 11788 MW; 8C35058CDC7749BC CRC64;

Query Match 37.7%; Score 468.5; DB 1; Length 109;
Best Local Similarity 81.2%; Pred. No. 5.4e-32;
Matches 91; Conservative 8; Mismatches 10; Indels 3; Gaps 1;

QY 21 EIVLTQSPGTLSPGERATLSCASQSVYDGDSDYNNWYQKPGQAPRLIYAASNLES 80
DB 1 EIVLTQSPGTLSPGERATLSCASQSVYDGDSDYNNWYQKPGQAPRLIYAASNLES 80
QY 81 GIPDRFSGSGGDTFTLTISRLEPEDFAVYCYQSQNSNEDPRTFGGKLEIKR 132
DB 58 GIPDRFSGSGGDTFTLTISRLEPEDFAVYCYQSQNSNEDPRTFGGKLEIKR 109

RESULT 13
KV3D_HUMAN
ID KV3D_HUMAN STANDARD; PRT; 129 AA.
AC P04207;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION CLL PRECURSOR (RHEUMATOID FACTOR).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86177570; PubMed=3083417;
RA Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,
RA Goldfien R., Carson D.A.;
RT "Cloning and sequence determination of a human rheumatoid factor
RT light-chain gene."
RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL; M12740; AA58992.1; -.
DR PIR; A01898; K3HUCU.
DR HSP; P01789; 2MCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION CLL.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT.
```

FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14275 MW; 5C13B411BE60CC14 CRC64;

Query Match 37.7%; Score 468.5; DB 1; Length 129;
Best Local Similarity 70.7%; Pred. No. 6.7e-32;
Matches 94; Conservative 15; Mismatches 19; Indels 5; Gaps 2;

QY 1 MEYDTILLWLLVWPGSTGEIVLTQSPGRLSLSPGERATLSCSKASQSDVDGDSYNNWY 60
DB 1 MEAPAQQLLLWLPDPTGTEIVMTQSPATLSVSPGERATLSCRSQSV-----SNNLAWY 56
QY 61 QOKPCQAPRLLIYAASNLGSGIPDRFSGSGTDTLTISRLEPEDFAVYCCQ-SNEDP 119
DB 57 QOKFCQPPRLLIYGASTRAITGIPARFSGSGTEFTLTISRLQSEDFAVYCCQINNWP 116

QY 120 RTFGQGTKEIKR 132
DB 117 WTFGGTRVEIKR 129

RESULT 14
KV3E_HUMAN STANDARD; PRT; 109 AA.
ID KV3E_HUMAN
AC P01623;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION WOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT group.";
RL Biochemistry 20:5816-5822(1981).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR; A01896; K3HWL.
DR HSP; P01789; 2WCP.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11746 MW; 566C115E6B9CBEE CRC64;

Query Match 37.4%; Score 464.5; DB 1; Length 109;
Best Local Similarity 82.1%; Pred. No. 1.2e-31;
Matches 92; Conservative 5; Mismatches 12; Indels 3; Gaps 1;

QY 21 EIVLTQSPGTLSPGERATLSCSKASQSDVDGDSYNNWYQOKPGQAPRLLIYAASNL 80
DB 1 EIVLTQSPGTLSPGERATLSCRSQSV---SSGILGWYQQKPGQAPRLLIYGASSRAT 57
QY 81 GIPDRFSGSGTDTLTISRLEPEDFAVYCCQSNEDPRTFGQGTKEIKR 132
DB 58 GIPDRFSGSGTDTLTISRLEPEDFAVYCCQYSGISLGRFTFGQGTKEIKR 109

RESULT 15
KV3L_MOUSE STANDARD; PRT; 111 AA.
ID KV3L_MOUSE
AC P01664;

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION CBPC 101.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01936; KVMSC1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11964 MW; E2BIAD98AD965962 CRC64;

Query Match 37.3%; Score 463; DB 1; Length 111;
Best Local Similarity 79.3%; Pred. No. 1.6e-31;
Matches 88; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 21 EIVLTQSPGTLSPGERATLSCSKASQSDVDGDSYNNWYQOKPGQAPRLLIYAASNL 80
DB 1 DIVLTQSPASLAVSLGORATISCKASQSDYTGESYNNWYQONPQSPKLLIYAASNL 60
QY 81 GIPDRFSGSGTDTLTISRLEPEDFAVYCCQSNEDPRTFGQGTKEIK 131
DB 61 GIPARFSGSGTDTLTINHPVEEDAATYYCCQSNEDPYTFGGGTKEIK 111

Search completed: April 17, 2002, 16:41:04
Job time: 172 sec

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RESULT 2
Q9RIAS
ID Q9RIAS PRELIMINARY; PRT; 214 AA.
AC Q9RIAS;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF152371; AAD40242.1; -.
DR HSP; P01789; IMCP.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR SMART; SM00410; IG_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR NON_TER 1
FT NON_TER 214
FT SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 55.6%; Score 691; DB 11; Length 214;
Best Local Similarity 59.2%; Pred. No. 2.3e-56;
Matches 129; Conservative 34; Mismatches 51; Indels 4; Gaps 1;

QY 21 EIVLTSPGTLSPGERATLSCASQSDYDGDSDSYNNWYQKPGQAPRLLIYAASNLES 80
Db 1 DIQLTSPSMYASLGERVTITCKASQDI----NSYLSWFQKPGKSPKTLIYRANLVD 56

QY 81 GIPDRFSGSGGDTFTLTISRLEPEDFVAVYCOQSNEDPRTFGQTKLEIKRTVAAPSVF 140
Db 57 GVPDRFSGSGGQDYSLTISSELYEDGIYCLQYDEFPETFGSGTKLEIKRAAAPTVS 116

QY 141 IFPPSEDLKSGTASVVCILNNPYPREAKVQWKVDNALQSGNSQESVTEGDSKDSSTYSLS 200
Db 117 IFPPSEQLTSGGASVCFVFNPNFYKDKINVKIDGSRQGVLSNWTDDSKDSTYSMS 176

QY 201 STLTLSKADYERKHVACEVTHOGLSPVTKSPNRGEC 238
Db 177 STLTLPKDEYERNSTYCEATHKTSPIVKCFNRNEC 214

RESULT 3
Q9UL78
ID Q9UL78 PRELIMINARY; PRT; 109 AA.
AC Q9UL78;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;

Query Match 35.0%; Score 434.5; DB 4; Length 109;
Best Local Similarity 77.7%; Pred. No. 6.2e-33;
Matches 87; Conservative 6; Mismatches 16; Indels 3; Gaps 1;

QY 21 EIVLTSPGTLSPGERATLSCASQSDYDGDSDSYNNWYQKPGQAPRLLIYAASNLES 80
Db 1 EIVLTSPGTLSPGERATLSCASQSV---SSSYLAWYQKPGQAPRLLIYGTSSRAT 57

QY 81 GIPDRFSGSGGDTFTLTISRLEPEDFVAVYCOQSNEDPRTFGQTKLEIKR 132
Db 58 GIPDRFSGSGGSETDFTLTISRLEPEDFVAVYCOQSGSSITFTFGPTKVDIKR 109

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RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035036; AAD56272.1; -.
DR HSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR NON_TER 1
FT NON_TER 109
FT SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 36.8%; Score 457.5; DB 4; Length 109;
Best Local Similarity 81.2%; Pred. No. 4.5e-35;
Matches 91; Conservative 5; Mismatches 13; Indels 3; Gaps 1;

QY 21 EIVLTSPGTLSPGERATLSCASQSDYDGDSDSYNNWYQKPGQAPRLLIYAASNLES 80
Db 1 EIVLTSPGTLSPGERATLSCASQSV---SSSYLAWYQKPGQAPRLLIYGTSSRAT 57

QY 81 GIPDRFSGSGGDTFTLTISRLEPEDFVAVYCOQSNEDPRTFGQTKLEIKR 132
Db 58 GIPDRFSGSGGDTFTLTISRLEPEDFVAVYCOQSGSSITFTFGPTKVDIKR 109

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RESULT 4
Q9UL86
ID Q9UL86 PRELIMINARY; PRT; 109 AA.
AC Q9UL86;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035028; AAD56264.1; -.
DR HSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR NON_TER 1
FT NON_TER 109
FT SEQUENCE 109 AA; 11928 MW; 243325F7C7DAC83 CRC64;

Query Match 35.0%; Score 434.5; DB 4; Length 109;
Best Local Similarity 77.7%; Pred. No. 6.2e-33;
Matches 87; Conservative 6; Mismatches 16; Indels 3; Gaps 1;

QY 21 EIVLTSPGTLSPGERATLSCASQSDYDGDSDSYNNWYQKPGQAPRLLIYAASNLES 80
Db 1 EIVLTSPGTLSPGERATLSCASQSV---SSSYLAWYQKPGQAPRLLIYGTSSRAT 57

QY 81 GIPDRFSGSGGDTFTLTISRLEPEDFVAVYCOQSNEDPRTFGQTKLEIKR 132
Db 58 GIPDRFSGSGGSETDFTLTISRLEPEDFVAVYCOQSGSSITFTFGPTKVDIKR 109

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SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 33.0%; Score 410; DB 4; Length 108;
Best Local Similarity 68.8%; Pred. No. 1.e-30;
Matches 77; Conservative 16; Mismatches 15; Indels 4; Gaps 1;

OY 21 EIVLTSPGTLSPGERATLSCKASQSVDYGDSYMNYQQKPGQAAPRLIYAASNLES 80
 ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
DB 1 DIQMTPSSSLSVSGDVRTITCRASQSI-----SYLWVYQKPKGNLLIYAASSLQS 56

OY 81 GPIDRSFGSGCTDTFTLTISRLEPDEFAVVYCQSNEDPRTFGGOTKLEIKR 132
 ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
DB 57 GVPSRFSGSGGTDFLTISLQLPDFAVYYCCYSYSTSWTFFGEGTKVEIKR 108

RESULT 7
O9UL83 PRELIMINARY; PRT; 108 AA.
AC O9UL83;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -! SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.


```
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF035033; AAD56269.1; -.
DR HSP; P80362; IWL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 30.6%; Score 380.5; DB 4; Length 107;
Best Local Similarity 65.2%; Pred. No. 6.1e-28;
Matches 73; Conservative 18; Mismatches 16; Indels 5; Gaps 2;

Qy 21 EIVTQSPGTLSPGERATLSCKASQSDYDGSYMNWYQKPGQAPRLIIYAASNLES 80
Db 1 DIQMTQSPSSLSASVGRVTITCRASQSI-----SNYLNWYQKPGKAPNLLIIYAASLSQS 56

Qy 81 GIPDRFSGSGTDFTLTISRLEPEDFVYVYCOQSNEDPRTFGQTKLEIKR 132
Db 57 GVPDRFSGSGTDFTLTISRLEPEDFVYVYCOQSNEDPRTFGQTKLEIKR 132

Qy 57 GVPDRFSGSGTDFTLTISRLEPEDFVYVYCOQSNEDPRTFGQTKLEIKR 132
Db 57 GVPDRFSGSGTDFTLTISRLEPEDFVYVYCOQSNEDPRTFGQTKLEIKR 132

RESULT 12
Q9JL80 PRELIMINARY; PRT; 103 AA.
AC Q9JL80;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus;
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF206026; AAF69324.1; -.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 103
SQ SEQUENCE 103 AA; 11224 MW; EC87D653DB3AAB21 CRC64;

Query Match 29.8%; Score 370; DB 11; Length 103;
Best Local Similarity 67.6%; Pred. No. 5.5e-27;
Matches 69; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

Qy 30 TSLSPGERATLSCKASQSDYDGSYMNWYQKPGQAPRLIIYAASNLESIGIPDRFSGS 89
Db 2 SLAVSLGQRATISCRASEVEYGTQKLMQYQKPGQAPRLIIYAASNVESGVPAFSGS 61

Qy 90 GSGTDFTLTISRLEPEDFVYVYCOQSNEDPRTFGQTKLEIKR 131
Db 62 GSGTDFSLNTHPVEEDDIAMFYCOQSRKVPWTFGGTKLEIKR 103

RESULT 13
Q9JL80
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ID Q9JL80 PRELIMINARY; PRT; 114 AA.
AC Q9JL80;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RC MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF035034; AAD56270.1; -.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 114
SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

Query Match 29.5%; Score 367; DB 4; Length 114;
Best Local Similarity 61.4%; Pred. No. 1.2e-26;
Matches 70; Conservative 21; Mismatches 21; Indels 2; Gaps 2;

Qy 21 EIVTQSPGTLSPGERATLSCKASQSDYDGSYMNWYQKPGQAPRLIIYAASNLE 79
Db 1 DVMTQSPSLPVLTRQPAISICRSSQSPVSDGTYLNWQKPGQAPRLIIYKVSNRD 60

Qy 80 SGIPDRFSGSGTDFTLTISRLEPEDFVYVYCOQSNEDPRTFGQTKLEIKR 132
Db 61 SGVPDRFSGSGTDFTLTISRLEPEDFVYVYCOQSNEDPRTFGQTKLEIKR 114

RESULT 14
Q9U410 PRELIMINARY; PRT; 106 AA.
AC Q9U410;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE MONOCLONAL ANTI-IDIDIOTYPIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN
VARIABLE REGION (FRAGMENT).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae;
OC Schistosoma.
OX NCBI_TaxID=6182;
RN 1
RP SEQUENCE FROM N.A.
RA Song X.T., Feng Z.O., Qiu Z.N., Li Y.O., Huang H.L., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the light chain
variable region gene of monoclonal anti-idiotypic antibody NP30 of
Schistosoma japonicum.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF207620; AAF19434.1; -.
DR HSP; P01679; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
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FT NON_TER 106 106
SQ SEQUENCE 106 AA; 11478 MW; F20F544426BAE63E CRC64;

Query Match      28.7%; Score 356.5; DB 5; Length 106;
Best Local Similarity 63.1%; Pred. No. 1e-25;
Matches 70; Conservative 12; Mismatches 24; Indels 5; Gaps 1;

QY 21 EIVLTQSPGTLSPGERATLSCAKSQSDYDGDSDYNNWYQKPGQAPRLIIYAASNLES 80
   | : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 1 ENLLTQSPALMSASPGKVTMTCSASSV-----SYVYVYLQKPGSSPRLIIYDTSNLAS 55

QY 81 GIPDRSGSGSGTDFLTITSLRLEPEDFAVYYCQSNEDPRTFGGKLEIK 131
   | : ||||| ||||| : ||||| || ||||| | ||||| | ||||| : |
Db 56 GVPVREGSGSGTSYSLTISRMEADAATYYCQQWTSYPFTFGSGTKLEIK 106

RESULT 15
Q9JL74 PRELIMINARY; PRT; 99 AA.
AC Q9JL74;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF206032; AAF69330.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
FT NON_TER 1 1
FT NON_TER 99 99
SQ SEQUENCE 99 AA; 10939 MW; 3B25D0E784533324 CRC64;

Query Match      27.3%; Score 339; DB 11; Length 99;
Best Local Similarity 64.4%; Pred. No. 3.9e-24;
Matches 65; Conservative 13; Mismatches 19; Indels 4; Gaps 1;

QY 31 LSLSPGERATLSCAKSQSDYDGDSDYNNWYQKPGQAPRLIIYAASNLESIPDRSGSG 90
   | : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 3 LLYSAGDRVTITCKASQSVNSD---VANWQQKPGSPKLLIYASNRYTGVDPRTGSG 58

QY 91 SGTFDTLTISRLEPEDFAVYYCQSNEDPRTFGGKLEIK 131
   ||||| ||||| : || ||||| | ||||| | ||||| : |
Db 59 YGTFDTTISTVQAEDLAVYFCQDYSSPRTFGGKLEIK 99
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Search completed: April 17, 2002, 16:40:41
Job time: 169 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 17, 2002, 16:38:53 ; Search time 40.38 Seconds
(without alignments)
862.171 Million cell updates/sec

Title: US-09-499-662-117
Perfect score: 2517
Sequence: 1 MGWSCIILFLVATATGVHSQ.....MHEALNNHYTKLSLSLSPCK 470

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_1101.*
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
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8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
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11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
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21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2517	100.0	470	AAW83037	Anti-Fas humanised
2	2517	100.0	470	AA114779	Humanised anti-Fas
3	2517	100.0	470	AAW90929	Humanised HFE7A de
4	2514	99.9	470	AAW90933	Humanised anti-Fas
5	2512	99.8	470	AAW90934	Humanised anti-Fas
6	2511	99.8	470	AAW90935	Humanised anti-Fas
7	2504	99.5	470	AAW83036	Anti-Fas humanised
8	2504	99.5	470	AA114776	Humanised anti-Fas
9	2504	99.5	470	AAW90926	Humanised HFE7A de
10	2498	99.2	470	AAW90936	Humanised HFE7A de
11	2301	91.4	652	AAW48650	Heavy chain of hma

12	2287.5	90.9	465	22	AAW72228	Humanised 323/A3 (
13	2287	90.9	470	21	AAW808026	A dimeric anti-CD2
14	2283	90.7	466	22	AAE03755	Chimeric 2403 IgG
15	2282.5	90.7	464	22	AAW72232	Humanised 323/A3 (
16	2252	89.5	476	20	AAW88464	Monoclonal antibody
17	2248.5	89.3	481	13	AAW24442	Sequence of antiHo
18	2245	89.2	472	20	AAW50166	Human reshaped F19
19	2229	88.6	449	14	AAW33339	Completely humanis
20	2229	88.6	449	19	AAW49816	Antibody D heavy c
21	2227	88.5	476	14	AAW31023	Ganglioside GM2 an
22	2226.5	88.5	583	22	AAW83156	Human immune syste
23	2199.5	87.4	467	22	AAW36210	Recombinant immuno
24	2197.5	87.3	452	20	AAW29458	Humanised anti-IL-
25	2197.5	87.3	452	21	AAW30322	Humanised anti-IL-
26	2197.5	87.3	452	21	AAW77766	Chimeric mouse/hum
27	2197	87.3	472	20	AAW50157	Amino acid sequenc
28	2190	87.0	592	22	AAW83838	Anti-IL-8 humanise
29	2188.5	86.9	452	19	AAW69316	Anti-5T4 single ch
30	2187	86.9	595	20	AAW86003	Human type antihum
31	2185.5	86.8	473	22	AAW84475	Human novel protei
32	2185	86.8	474	22	AAU14177	Human type antihum
33	2182.5	86.7	473	22	AAW64471	Human type antihum
34	2177.5	86.5	473	22	AAW64469	Human type antihum
35	2174	86.4	468	20	AAW85689	D9D10 heavy chain
36	2174	86.4	711	20	AAW85692	MoTABII fusion pro
37	2170.5	86.2	473	22	AAW84473	Human type antihum
38	2159	85.8	470	13	AAW22757	Reshaped CAMPATH-1
39	2157.5	85.7	453	20	AAW50151	Antibody F19 chime
40	2155	85.6	472	17	AAW93166	Anti-rhesus D reco
41	2152.5	85.5	454	14	AAW30774	H52H4-160 murine a
42	2146.5	85.3	467	13	AAW22758	Reshaped CD4 antib
43	2142.5	85.1	467	13	AAW22759	Human novel protei
44	2142.5	85.1	477	22	AAU14288	Sequence encoded b
45	2139	85.0	466	14	AAW40750	

ALIGNMENTS

RESULT	1
AAW83037	AAW83037 standard; Protein; 470 AA.
ID	AAW83037 standard; Protein; 470 AA.
XX	AAW83037;
XX	15-MAR-1999 (first entry)
DT	Anti-Fas humanised antibody HFE7A heavy chain.
XX	HFE7A; monoclonal antibody; mouse; Fas; humanised antibody; apoptosis; HFE7A; autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.
XX	Homo sapiens.
OS	Synthetic.
XX	Key Location/Qualifiers
FT	Peptide 1..19
FT	Protein /label= Sig_peptide
FT	Region /label= Mat_protein
FT	Region /label= Variable
FT	Region /label= Constant

FT	Region	50..54	
FT		/label= CDR_H1	
FT		/note= "claim 9"	
FT	Region	69..84	
FT		/label= CDR_H2	
FT		/note= "claim 9"	
FT	Region	118..129	
FT		/label= CDR_H3	
FT		/note= "claim 9"	
XX	AAU959701-A.		
PN			
XX	08-OCT-1998.		
XX			
XX	30-MAR-1998;	98AU-0059701.	
XX			
PR	08-OCT-1997;	97JP-0276064.	
PR	01-APR-1997;	97JP-0082953.	
PR	25-JUN-1997;	97JP-0169088.	
XX			
XX	(SANY) SANKYO CO LTD.		
XX			
PI	Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;		
PI	Masahiko O, Nobufusa S, Shin Y, Tohru Y;		
XX			
DR	N-PSDB; AAU70080.		
DR			
XX			
PT	New antibodies and proteins bind conserved epitope of Fas antigen -		
PT	used to evaluate drugs in animal models and to treat Fas-associated		
PT	diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,		
PT	myocarditis, hepatitis and AIDS		
XX			
PS	Claim 22; Page 225-227; 292pp; English.		
XX			
CC	This is the amino acid sequence of the HV type humanised heavy		
CC	chain of murine anti-human Fas monoclonal antibody HFE7A. It		
CC	includes humanising R44G and A76T amino acid substitutions that are		
CC	are conserved in the human IgG heavy chain. Host Escherichia coli		
CC	pGHPDHV3 SANK 70298 harbors plasmid pGHPDHV3 carrying a fusion		
CC	fragment of the humanised HV type HFE7A heavy chain and DNA		
CC	encoding human IgG1 constant region (see AAU70080), and is deposited		
CC	as FRM BP-6273 (claimed). The invention provides methods for		
CC	producing humanised antibodies by culturing host cells. Humanised		
CC	versions of HFE7A (see AAU83031-37), like native HFE7A, are capable		
CC	of inducing apoptosis in abnormal cells expressing Fas, and of		
CC	inhibiting Fas-induced apoptosis in normal cells. The humanised		
CC	antibodies are used to evaluate, in animal models, treatments of		
CC	diseases that involve Fas/Fas ligand interactions, and also to		
CC	treat such diseases, including autoimmune disease (e.g. systemic		
CC	lupus erythematosus, Hashimoto's disease, graft versus host disease,		
CC	Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,		
CC	Goodpasture syndrome, Crohn's disease, rheumatoid arthritis,		
CC	autoimmune haemolytic anaemia, sterility, myasthenia gravis,		
CC	multiple sclerolosis, Basedow's disease, thrombopenia purpura and		
CC	insulin-dependent diabetes), allergies, atopy, arteriosclerosis,		
CC	myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic		
CC	anaemia, hepatitis, AIDS and transplant rejection (all claimed).		
XX			
SQ	Sequence 470 AA;		
Query Match 100.0%; Score 2517; DB 19; Length 470;			
Best Local Similarity 100.0%; Pred. No. 9, 2e-145;			
Matches 470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	MGWSCIIFLVATATGTVHVSQVLQSGAEVKKPGASVKVSKASGYTFTSYMMQWKQAP 60	
Db	1	mgwsciiflvatgvtghvsqvlvqsgaevkkpgasvkvsckasgytftsymqwkqap 60	
QY	61	GGGLEWNGETDPDSDSYNNQKFKGKATLVDTSTAYMELSLRSEDYVYCARNRD 120	
Db	61	ggglewngelddpsdysnynnqkfkgtkaltvdtstaymelsslrsedtavvyccarnrd 120	

CC the treatment or prevention of conditions such as autoimmune diseases,
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 CC and organ graft rejection. Sequences AAB14775-B14776 and AAB14779
 CC represent the heavy chains (or fragments thereof) of various humanised
 CC HFE7A-derived anti-Fas antibodies.
 XX
 SQ Sequence 470 AA;

Query Match 100.0%; Score 2517; DB 21; Length 470;
 Best Local Similarity 100.0%; Pred. No. 9.2e-145;
 Matches 470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSCIIILFLVATATGVHSQVQLVSGAEVKKPGASVKVSKASGYTFTSYMQWVKQAP 60
 DB 1 mgwsciiilflvatatgvhsqvlvgdgaevkkpgasvkvsckasgytftsyvmqwkqap 60
 QY 61 GGLGEMGEIDPSDSYTNVYNOKFKGKATLTVDSTSTAYMELSSLSRSEDVAVYCARND 120
 DB 61 ggglewmgeidpsdsytnynkfkgkatltvdstststaymelsslsrsetavvycarnrd 120
 QY 121 YSNNNYFDVWCGTGLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVYS 180
 DB 121 ysnnyfvdwvgtgltvtvssastkgpsvfplapskstsggtaalgclvkdyppeptvys 180
 QY 181 WNSGALTSGVHTFPVAVLQSSGLYSLSSVVVTPSSSLGTQTYICNVNHKPSNTKVDKRVEP 240
 DB 181 wnsгалtsгvhtfpavlqssglyslssvvvtpssslgtqtyicnvnhkpsntkvdkrvep 240
 QY 241 KSCDKTHCPCCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
 DB 241 kscdkthcpccpapeilggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw 300
 QY 301 YVDGVEVHNAKTPREQYNSTYRVVSVLTVHLQDMLAGKEYCKVKCNKALPAPIEKTIS 360
 DB 301 yvdgvevhnaktpreeqynstyrvvsvltvhlqdgmlagkeyckvkcnkalpapiektis 360
 QY 361 KAKGPDPQVYTLPPSREMTKNOVSLTCLVKGYFDPYSDIAVEWESNQPENNYKTTTPV 420
 DB 361 kagkdpdpqvylppsremtknovsltclvkgyfdpydsdiavewesngqpennyykttppv 420
 QY 421 LDSGSEFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSLSPGK 470
 DB 421 ldsгsefflyskltvdksrwqgnvfссvmhealhnhytklslsлspgk 470

RESULT 3
 ID AAW90929 standard; Protein; 470 AA.
 AC AAW90929;
 XX
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Humanised HFE7A designed heavy chain protein #2.

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antifertility; neuroprotective; antiatherosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX Synthetic.
 OS
 XX
 XX EP990663-A2.
 XX

PD 05-APR-2000.
 XX 29-SEP-1999; 99EP-0307711.
 XX 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.
 XX (SANY) SANKYO CO LTD.
 PA Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 PI WPI: 2000-258930/23.
 DR N-PSDB; AAA11622.
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems -
 PS Example reference 22; Page 150-152; 263pp; English.
 XX This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antifertility, neuroprotective,
 CC antiarteriosclerotic, cardiac and hepatotropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Sjogren's syndrome, rheumatoid arthritis, graft
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A designed heavy chain which is used in
 CC the method described in the invention.
 XX
 SQ Sequence 470 AA;

Query Match 100.0%; Score 2517; DB 21; Length 470;
 Best Local Similarity 100.0%; Pred. No. 9.2e-145;
 Matches 470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSCIIILFLVATATGVHSQVQLVSGAEVKKPGASVKVSKASGYTFTSYMQWVKQAP 60
 DB 1 mgwsciiilflvatatgvhsqvlvgdgaevkkpgasvkvsckasgytftsyvmqwkqap 60
 QY 61 GGLGEMGEIDPSDSYTNVYNOKFKGKATLTVDSTSTAYMELSSLSRSEDVAVYCARND 120
 DB 61 ggglewmgeidpsdsytnynkfkgkatltvdstststaymelsslsrsetavvycarnrd 120
 QY 121 YSNNNYFDVWCGTGLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVYS 180
 DB 121 ysnnyfvdwvgtgltvtvssastkgpsvfplapskstsggtaalgclvkdyppeptvys 180
 QY 181 WNSGALTSGVHTFPVAVLQSSGLYSLSSVVVTPSSSLGTQTYICNVNHKPSNTKVDKRVEP 240
 DB 181 wnsгалtsгvhtfpavlqssglyslssvvvtpssslgtqtyicnvnhkpsntkvdkrvep 240
 QY 241 KSCDKTHCPCCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
 DB 241 kscdkthcpccpapeilggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw 300

Db 241 kscdtkhtccpccpapellgpgsvflfppkpkdtlmierptvctvvvdshdpevkfnw 300
 QY 301 YVDGVEVHNKATKPREQYNTYRVSVSLTVLHQDWLNGKEYCKVSNKALPAPIERTIS 360
 Db 301 yvdgvevhnaktkpreeqynstyrsvsltlvlhqdwlngkeyckvsnkalpapiertis 360
 QY 361 KAKQPREPQVYTLPPSREMTKNQVSLTCLVKGFFYSDIAVESNGQPNNYKTPPV 420
 Db 361 kagqprepqvytlppsreemtknqvaltclvkgfypsdiavesngqpennyktppv 420
 QY 421 LDSGSPFLYSKLTVDKSRWQOGNVFSCVMHEALHNHYTKSLSPGK 470
 Db 421 ldsdgsfplyskltvdksrwqggnvfscvmhealhnhytqkslspgk 470

RESULT 4
 AAW90933
 ID AAW90933 standard; Protein; 470 AA.
 AC AAW90933;
 XX 08-AUG-2000 (first entry)
 DT Humanised anti-Fas designed heavy chain Heu 1 protein.
 DE
 XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatologic; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX Synthetic.
 OS
 XX EP990663-A2.
 PN
 XX 05-APR-2000.
 PD
 XX 29-SEP-1999; 99EP-030711.
 PF
 XX 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.
 XX
 XX (SANY) SANKYO CO LTD.
 PA
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 PI WPI: 2000-258930/23.
 XX N-PSDB; AAA11644.
 DR
 XX

New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems

Claim 2; Page 169-170; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral, immunomodulatory, dermatologic, immunosuppressive, thyromimetic, antirheumatic, nephrotropic, antiinfertility, neuroprotective, antiarteriosclerotic, cardiant and hepatotropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic

CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody heavy chain construct designated Heu 1 which is described in the method of the invention.

XX Sequence 470 AA;

Query Match 99.9%; Score 2514; DB 21; Length 470;
 Best Local Similarity 99.8%; Pred. No. 1.4e-144;
 Matches 469; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSCIIILFVATATGVHSQVLVQSGAEVKKPGASVKVSKASGYTFTSYMMQWVKQAP 60
 Db 1 mgwsciiilfvatgvtghsqvqlvgsgaevkpgasvkscasgytftsymbwvkqap 60
 QY 61 GQGLEWGEIDPDSYNYNOKFKGKATLTVDTSSTAYMELSLRSEDFTAVYCARNRD 120
 Db 61 gqglewgeidpdsytnynqkfkgtltvdtststaymelslrseftavycarnrd 120
 QY 121 YSNWYFDVMGEGFLTVSVASASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS 180
 Db 121 ysnwfydvmgqgtltvsvsaastkgpsvfplapsskstsggtaalgclvdyfpeptvs 180
 QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNKKPSNKKVDRKVEP 240
 Db 181 wnsгалtsgvhtfpavlgssglyslssvvtvpssslgtqtyicnvnhkpsnkvdkrvep 240
 QY 241 KSCDKTHTCTPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
 Db 241 kscdkthctpcpapellggpsvflfppkpkdtlmisrtpevtcvvvdshdpevkfnw 300
 QY 301 YVDGVEVHNKATKPREQYNTYRVSVSLTVLHQDWLNGKEYCKVSNKALPAPIERTIS 360
 Db 301 yvdgvevhnaktkpreeqynstyrsvsltlvlhqdwlngkeyckvsnkalpapiertis 360
 QY 361 KAKQPREPQVYTLPPSREMTKNQVSLTCLVKGFFYSDIAVESNGQPNNYKTPPV 420
 Db 361 kagqprepqvytlppsreemtknqvaltclvkgfypsdiavesngqpennyktppv 420
 QY 421 LDSGSPFLYSKLTVDKSRWQOGNVFSCVMHEALHNHYTKSLSPGK 470
 Db 421 ldsdgsfplyskltvdksrwqggnvfscvmhealhnhytqkslspgk 470

RESULT 5

AAW90934

ID AAW90934 standard; Protein; 470 AA.

XX AAW90934;

XX 08-AUG-2000 (first entry)

DE Humanised anti-Fas designed heavy chain Heu 2 protein.

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatologic; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;

Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 Synthetic.
 OS EP990663-A2.
 PN 05-APR-2000.
 PD 29-SEP-1999; 99EP-0307711.
 PF 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.
 XX (SANY) SANKYO CO LTD.
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 WPI: 2000-258930/23.
 DR N-PSDB; AAA11645.
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 inflammatory or autoimmune disease, induces apoptosis selectively in
 cells with abnormal Fas-Fas ligand systems -
 Claim 2 : Page 174-176; 263pp; English.
 This invention describes a novel humanized anti-Fas antibody-like
 molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 ligand system, by binding to Fas on the cell surface, and prevents
 apoptosis in cells with a normal system, by inhibiting binding between
 Fas and its ligand. The products of the invention have anti-inflammatory,
 immunomodulatory, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 antirheumatic, dermatological, immunosuppressive, thyromimetic,
 antihypertensive, nephrotropic, antifertility, neuroprotective,
 antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 apoptosis by binding to cell surface Fas or inhibit it by competitive
 inhibition of ligand binding. (I) are used to treat and/or prevent
 diseases associated with the Fas/Fas ligand system, especially systemic
 lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 versus host disease, Sjogren's syndrome, pernicious or hypoplastic
 anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 inhibit apoptosis in normal cells but selectively induce it in abnormal
 cells. They bind to both human and murine Fas, so can be evaluated in
 murine disease models. (I) act on the active site of Fas, i.e. they mimic
 the native ligand, do not induce liver disease, and have reduced risk of
 inducing a human anti-murine antibody response. This sequence represents
 a humanised anti-Fas antibody heavy chain construct designated Heu 2
 which is described in the method of the invention.
 Sequence 470 AA;
 Query Match 99.8%; Score 2512; DB 21; Length 470;
 Best Local Similarity 99.6%; Pred. No. 1.9e-144;
 Matches 468; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGWSCIILFVATATGVHVSQVLSGAEVKKPGASVKVSKASGYTFTSYWQWVKQAP 60
 DB 1 mgwscilflvatatgvhsqvlsgaevkkpgasvskcasgytftsywmqwrkqap 60
 QY 61 GQGLEWMEIDSDSYTNTNQKFKATLTVDTSSTAYWELSSURSEDATVYYCARNRD 120
 DB 61 gqglewmeidpsdsytnynqkfkattitvdtsstaymelslrsedatvyyccarnrd 120
 QY 121 YSNNNYFDWVGECTLVTVSSASTKGSVPFLAPSSKSTSGGTAALGCLIKDYFPEPVTVS 180

DB 121 ysnnnwföwggcllvtvssastkgsvpflapsskstsggtaalgclvkdypcvts 180
 QY 181 WNSGALTSVHTFPAYLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHPKSTKVDKRVPEP 240
 DB 181 wnsгалtsvhtfpavlyqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkrvep 240
 QY 241 KSCDKTHTCPCPAPPELLGPGSPVFLPPPKDITLMSIRPPEVTCVVVDVSHEDPEVKFNW 300
 DB 241 kscdkthtccpccpapellgpgsvflpppkdtlmsirtpcvtcvvdvshedpevkfnw 300
 QY 301 YVDCVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIIS 360
 DB 301 yvdgvevhnaaktprceeqynstyrvvsvlvtlvhqdwlngkeyckvsnkalpapiektis 360
 QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPV 420
 DB 361 kagqprepqvtytlppsreemtqnvsltcclvkgyfypsdiavewesngqpennnykttppv 420
 QY 421 LQDSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 470
 DB 421 ldsdgsfflyskltvdksrwqgnvfscsvmhealhnhytqkslsispgk 470
 RESULT 6
 AAW90935 standard; Protein; 470 AA.
 XX ID AAW90935;
 AC AAW90935;
 XX 08-AUG-2000 (first entry)
 DT Humanised anti-Fas designed heavy chain Heu 3 protein.
 DE Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antifertility; neuroprotective; antarteriosclerotic;
 KW hepatotropic; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 OS Synthetic.
 XX EP990663-A2.
 PN 05-APR-2000.
 PD 29-SEP-1999; 99EP-0307711.
 PF 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.
 XX (SANY) SANKYO CO LTD.
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 WPI: 2000-258930/23.
 DR N-PSDB; AAA11646.
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 inflammatory or autoimmune disease, induces apoptosis selectively in
 cells with abnormal Fas-Fas ligand systems -
 Claim 2: Page 180-182; 263pp; English.
 This invention describes a novel humanized anti-Fas antibody-like
 molecule (I) that, induces apoptosis in cells with an abnormal Fas/
 ligand system, by binding to Fas on the cell surface, and prevents


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CC treat such diseases, including autoimmune disease (e.g. systemic
CC lupus erythematosus, Hashimoto's disease, graft versus host disease,
CC Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,
CC autoimmune haemolytic anaemia, Crohn's disease, rheumatoid arthritis,
CC autoimmune haemolytic anaemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura and
CC insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
XX
SQ Sequence 470 AA;
Query Match 99.5%; Score 2504; DB 19; Length 470;
Best Local Similarity 99.6%; Pred. No. 5.7e-144;
Matches 468; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MGWSCIIILFLVATATGVHSQVLQSGAEVKKPGASVKVSKRASKGYTFTSYMQWVKQAP 60
DB 1 mgwsciiilflvatatgvhsqvlqsgaevkpgasvkksckasgytftsymwvkvqap 60
QY 61 GQGLEWMEIDSDSYTNYNQKFKGKATLVDFTSTAYMELSSLRSEDVAVYYCARNRD 120
DB 61 gqglewmgeidpsdysytnynqkfkgtlvtvdsasaymelsslrseavyyccarnrd 120
QY 121 YSNNNYFDVWGEGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS 180
DB 121 ysnnnfydvwgegltvvtssastkgpsvfpplapskstsaggtaalgclvdyfpeptvs 180
QY 181 WNSGALTSVGHFTFPVAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHNKPSNTKVDKRVEP 240
DB 181 wnsгалtsvghftfpavqlqssglsylssvvtvppssslgtqtyicnvnhkpsntkvdkrvep 240
QY 241 KSCDKTHTCCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
DB 241 kscdkthtccpcpapellggpsvflfppkpkdtlmsrtpevtcvvvdvshedpevkfnw 300
QY 301 YVDGVEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
DB 301 yvdgvevhnaktpreeqynstyrvvsvltvlhqdwlngkeyckcvsnkalpapiektis 360
QY 421 LDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTKQSLSPGK 470
DB 421 ldsdgsfflyskltvdksrwqgnvfscsvmhealhnytkqslslspgk 470
RESULT 8
AAB14776
ID AAB14776 standard; Protein; 470 AA.
XX
AC AAB14776;
XX
DT 24-NOV-2000 (first entry)
XX
DE Humanised anti-Fas antibody heavy chain, SEQ ID NO:89.
KW murine; humanised antibody; monoclonal antibody HFE7A; FERM-BP-5828;
KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;
KW hepatitis; AIDS; graft rejection; heavy chain.
XX
OS Chimeric - Mus musculus.
OS Chimeric - Homo sapiens.
XX
FN JP2000169393-A.
XX
PD 20-JUN-2000.
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XX 30-SEP-1999; 99JP-0278301.
XX 30-SEP-1998; 98JP-0276883.
XX (SANY ) SANKYO CO LTD.
XX WPI; 2000-485645/43.
XX N-PSDB; AAA72159.
XX Preventive or treating agent for the diseases caused by an abnormality
XX in the Fas/Fas ligand system e.g. autoimmune diseases, contains
XX anti-Fas antibody
XX Claim 21; Page 95-96; 139pp; Japanese.
XX The invention relates to compositions for the prevention or treatment
XX of diseases caused by an abnormality in the Fas/Fas ligand system
XX containing an anti-Fas antibody as the active component. The anti-Fas
XX antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
XX or a humanised version of HFE7A containing identical CDRs
XX (complementarity determining regions) to antibody HFE7A. Via its
XX interaction with Fas, the antibody of the invention acts as a modulator
XX of apoptosis. The composition of the invention may therefore be used in
XX the treatment or prevention of conditions such as autoimmune diseases,
XX allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
XX glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
XX and organ graft rejection. Sequences AAB14775-B14776 and AAB14779
XX represent the heavy chains (or fragments thereof) of various humanised
XX HFE7A-derived anti-Fas antibodies.
XX Sequence 470 AA;
Query Match 99.5%; Score 2504; DB 21; Length 470;
Best Local Similarity 99.6%; Pred. No. 5.7e-144;
Matches 468; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MGWSCIIILFLVATATGVHSQVLQSGAEVKKPGASVKVSKRASKGYTFTSYMQWVKQAP 60
DB 1 mgwsciiilflvatatgvhsqvlqsgaevkpgasvkksckasgytftsymwvkvqap 60
QY 61 GQGLEWMEIDSDSYTNYNQKFKGKATLVDFTSTAYMELSSLRSEDVAVYYCARNRD 120
DB 61 gqglewmgeidpsdysytnynqkfkgtlvtvdsasaymelsslrseavyyccarnrd 120
QY 121 YSNNNYFDVWGEGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS 180
DB 121 ysnnnfydvwgegltvvtssastkgpsvfpplapskstsaggtaalgclvdyfpeptvs 180
QY 181 WNSGALTSVGHFTFPVAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHNKPSNTKVDKRVEP 240
DB 181 wnsгалtsvghftfpavqlqssglsylssvvtvppssslgtqtyicnvnhkpsntkvdkrvep 240
QY 241 KSCDKTHTCCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
DB 241 kscdkthtccpcpapellggpsvflfppkpkdtlmsrtpevtcvvvdvshedpevkfnw 300
QY 301 YVDGVEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
DB 301 yvdgvevhnaktpreeqynstyrvvsvltvlhqdwlngkeyckcvsnkalpapiektis 360
QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420
DB 361 kkgqprepqvylppsreemtknqvsltclvkgyfypsdiavewesngqpennnykttppv 420
QY 421 LDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTKQSLSPGK 470
DB 421 ldsdgsfflyskltvdksrwqgnvfscsvmhealhnytkqslslspgk 470
RESULT 9
AAB90926
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XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 XX WPI: 2000-258930/23.
 DR N-PSDB; AAA11655.
 XX
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems
 XX Claim 2; Page 188-189; 263pp; English.
 XX
 CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antiinfectility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto's disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A heavy chain construct HHH type
 CC which is described in the method of the invention.
 XX Sg Sequence 470 AA;

Query Match 99.28; Score 2498; DB 21; Length 470;
 Best Local Similarity 98.98; Pred. No. 1.3e-143;
 Matches 465; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MGWSCIIILFLVATATGVHRSQVLQSGAEVKKPGASVKVSKASGYTFTSYMMQWVKQAP 60
 Db 1 mgwsciiilflvatatgvhsqvlqsgaevkkpgasvkvsckasgytftsyymmqrqap 60

Qy 61 GQGLEWNGEIDPSYNYNOKFKGKATLVDTSTSTAYMELSLRSEDATVYYCARNRD 120
 Db 61 gqglewngeidpsdysnyngkfgrvtitrtststaymelslrsedsatvyyccarnrd 120

Qy 121 YSNWNYDVWCEGLTVVSSASTGPSVFLAPSSKTSFGTAAAGCLVLDYFPEPTVVS 180
 Db 121 ysnwnydvwceglvtvssastgpsvflapssktsfgttaaagclvldyfppeptvvs 180

Qy 181 WNSGALTSVGHVTPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNKHPSNTKVDKRVPE 240
 Db 181 wnsгалtsvghvtpavllqssglyslssvstvtpssslgtqtyicnvnhkpsntkvdkrvpe 240

Qy 241 KSCDKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
 Db 241 kscdkhtcpcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw 300

Qy 301 YVDCGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIIS 360
 Db 301 yvdcgvevhnatkpreeqynstyrvvsvltvlhqdwlngkeyckvsnkalpapieltis 360

Qy 361 KAKGQPREPPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEVESNGQPENNYKTTTPPV 420
 Db 361 kkgqpreppvytlpppreemtknqvsltclvkgyfypsdiavevesngqpennnykttppv 420

Db 361 kkgqpreppvytlpppreemtknqvsltclvkgyfypsdiavevesngqpennnykttppv 420

Qy 421 LDSGGSFLYLSKLTVDKSRWQGNVFSVSMHEALHNHYTKLSLSPOK 470
 Db 421 ldsdgsfflylskltvdksrwqgnvfscvsmhealhnhytqklslspsgk 470

RESULT 11
 AAW48650
 ID AAW48650 standard; Protein; 652 AA.
 XX
 AC AAW48650;
 XX
 DT 04-AUG-1998 (first entry)
 XX
 DE Heavy chain of hmAb425 fused to TNF alpha.
 XX
 KW Antibody-cytokine fusion protein; tricitronic vector; chimeric;
 KW TNF alpha; IL-2; IRES; internal ribosome entry site.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..494
 FT /note= "Heavy chain of human mAb 425"
 FT Region 495..652
 FT /note= "TNF alpha"
 FT
 FT WO9811241-A1.
 XX
 PD 19-MAR-1998.
 XX
 PF 02-SEP-1997; 97WO-EP04765.
 XX
 PR 30-SEP-1996; 96EP-0115635.
 PR 16-SEP-1996; 96EP-0114820.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Bruemmer W, Burge C, Dunker R, Hauser H, Mielke C;
 PI Rieke E, Von Hoegen I, Welge T;
 XX
 DR WPI: 1998-207400/18.
 DR N-PSDB: AAV18096.
 XX
 PT Oligo:citrionic expression vector - useful for production of, e.g.
 PT MAB425/TNF-^a or MAB425/IL-2 antibody fusion protein
 XX
 PS Disclosure; Fig 15; 89pp; English.
 XX
 CC The present sequence represents a fusion protein comprising of TNF
 CC alpha fused to the C-terminus of the heavy chain of the human
 CC monoclonal antibody 425 (hmAb425). The hmAb425 has specificity for
 CC the human EGF receptor. The invention claims for a new PMCLDHAP
 CC tricitronic vector (AAV18096) for the expression of an
 CC antibody-cytokine fusion protein, hmAb425-TNF alpha. The TNF alpha
 CC sequence can be substituted by the IL-2 sequence. The vector also
 CC contains a strong promoter/enhancer unit, a selection marker gene and at
 CC least two poliovirus derived internal ribosomal entry site (IRES)
 CC sequences. The vector can be expressed in mammalian host cells for the
 CC production of heteromeric fusion proteins. This expression system is
 CC claimed to produce the heteromeric proteins in high yields.
 XX
 Sg Sequence 652 AA;

Query Match 91.48; Score 2301; DB 19; Length 652;
 Best Local Similarity 87.98; Pred. No. 1.5e-131;
 Matches 435; Conservative 17; Mismatches 17; Indels 26; Gaps 3;

Qy 1 MGWSCIIILFLVATATGVHRSQVLQSGAEVKKPGASVKVSKASGYTFTSYMMQWVKQAP 60
 Db 1 mgwsciiilflvatatgvhsqvlqsgaevkkpgasvkvsckasgytftsyymmqrqap 60

Db 1 mdwtvrvfcllavapaghsqvlvqsgaevkkgasvkvscasgytftshmhvrrqap 60
QY 61 GQLEWMEIDPDSYTNQKFKGKATLTVDSTSTAYMELSLRSDDTAVYYCARNRD 120
Db 61 gqglewgefnpsngrtnynekfkskmtvtstntaymelslrsddtavyycasrd 119
QY 121 YS-NNWTFDVGEGTLTVSS-----ASTKGPSVPLAPSS 155
Db 120 ydydgrfydgqgltvtvssgewilcawaqlcptprshgttslaastkgspsvflapss 179
QY 156 KSTSGGTAAALGCLVKDYFPEPTVSNWNGALTSGVHHPFAVLQSSGLYSLSSVTVTPSSS 215
Db 180 kstsggtaalgclvkdypfpvptvsnwngaltsgvnhlfpavlgsglyslssvvtvpsss 239
QY 216 LGTQTYICNVNHNKPSNTKVRPKCDKTHTCPPCPAPELLGGPSVFLFPPPKDPTLM 275
Db 240 lgtqtyicnvnhkpsntckvdkkvepkcdkthtcppcpapeellggpsvflfppkpkdtlm 299
QY 276 ISRTPEVTCVVVDYSHEDPEVKFNWYVDGVEVHNKATKPREEQYNSTYRVVSVLTVLHQD 335
Db 300 isrtpevtcvvdvshedpevkfnwyvdgvevhnaktkpreegynstyrvsvltvlhqd 359
QY 336 WLNGKEYCKVSKNKAAPAEKTIKSKAKGQPREPQVYTLPPSRREMTKNQVSLTCLVKGF 395
Db 360 wlngkeyckvsknkalpaeiktiskakgqprepqvylppsrdeltknqvsltclvkgf 419
QY 396 YPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL 455
Db 420 ypsdiawesngqpennnykttpvldsgsfflyskltvdkswqgnvfscsvmhheal 479
QY 456 HNHYTQKSLSLSPGK 470
Db 480 hnhytqkslspsgk 494

RESULT 12

AAB72228
ID AAB72228 standard; Protein; 465 AA.

XX
AC AAB72228;

XX
DT 10-MAY-2001 (first entry)

XX
DE Humanised 323/A3 (IgG1) antibody heavy chain amino acid sequence.

XX
KW Anti-Ep-CAM antibody; cyclic adenosine monophosphate; cell synthesis;
KW chemotherapeutic agent; cytostatic; anti-cancer therapy; cancer;
XX heavy chain.

XX
OS Mus sp.

XX
OS Homo sapiens.

XX
PN WO200107082-A1.

XX
PD 01-FEB-2001.

XX
PF 23-JUL-1999; 99WO-EP05271.

XX
PR 23-JUL-1999; 99WO-EP05271.

XX
PA (GLAX) GLAXO GROUP LTD.

XX
PI Knick VC, Stimmel JB, Thurmond LM;

XX
DR WPI; 2001-182729/18.

XX
DR N-PSDB; AAF63374.

XX
PT Combination for treating cancer (e.g. breast, gastric or prostate
PT cancers), or in the manufacture of a medicament for anti-cancer
PT therapy, comprises an anti-Ep-cyclic adenosine monophosphate antibody
PT with a chemotherapeutic agent -
XX
XX Disclosure; Fig 16; 103pp; English.

XX

CC This invention relates to a combination of an anti-Ep-CAM (cyclic
CC adenosine monophosphate) antibody with a chemotherapeutic agent, that is
CC capable of arresting Ep-CAM antigen expressing cells in the synthesis (S)
CC phase or the second growth phase (M) of cell enlargement (G2)/DNA
CC replication. The antibody exhibits cytostatic activity and is useful in
CC the manufacture of a medicament for use in anti-cancer therapy,
CC characterised in that a chemotherapeutic agent, which is capable of
CC arresting Ep-CAM antigen expressing cells in S or in G2/M, is
CC co-administered to a patient with an anti-Ep-CAM antibody. The
CC combination is useful for treating cancer, particularly colorectal
CC cancer, breast cancer, gastric cancer, prostate cancer or non-small-cell
CC lung cancer. The present sequence represents the heavy chain of
CC anti-Ep-CAM antibody known as humanised 323/A3 (IgG1) which can be used
CC in the combination of the invention.

XX Sequence 465 AA;

Query Match 90.9%; Score 2287.5; DB 22; Length 465;
Best Local Similarity 91.7%; Pred. No. 6.9e-131;
Matches 431; Conservative 14; Mismatches 20; Indels 5; Gaps 2;

QY 1 MGWSCIIILFLVATATGSHVQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKQAP 60

Db 1 mgwsciiilflvatatgshvqvlvqsgaevkpgasvkvsckasgytftfnygmwnvrrqap 60

QY 61 GQLEWMEIDPDSYTNQKFKGKATLTVDSTSTAYMELSLRSDDTAVYYCARNRD 120

Db 61 gqglewmgwintygeptygedfkgfaisldtsastaymelslrsddtavyfcar--- 117

QY 121 YSNWYFDVWMEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVTS 180

Db 118 fgn--yydywgqgslvtvssastkgpsvfplapsskstsggtaalgclykdyfpeptvts 175

QY 181 WNSGALTSGVHTFPVAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKRVPE 240

Db 176 wnsгалtsgvhtfpavlgssglyslssvtpssslgtqtyicnvnhkpsntkvdkkvpe 235

QY 241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300

Db 236 kscdkthtcppcpapeellggpsvflfppkpkdtlmisrtpevtcvvdvshedpevkfnw 295

QY 301 YVDGVEVHNARTKPREEQYNSTYRVWSVLTVLHQDLNKGKEYCKVSKNKAAPAEIKTIS 360

Db 296 yvdgvevhnartkpreeqynstyrvsvltvlhqdwingkeyckvsknkalpaeiktis 355

QY 361 KAKGQPREPQVYTLPPSRREMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420

Db 356 kagqprepqvylppsrdeltnqvaltclvkgfypsdiawesngqpennkyttppv 415

QY 421 LDSGSPFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470

Db 416 ldsdgsfllyskltvdkswqgnvfscsvmhhealhnhytqkslspsgk 465

RESULT 13

AAB08026

ID AAB08026 standard; Protein; 470 AA.

XX
AC AAB08026;

XX
DT 14-NOV-2000 (first entry)

XX
DE A dimeric anti-CD20 heavy chain polypeptide.

XX
KW Anti-CD20 antibody; dimeric immunoglobulin; immunoglobulin; IgG;
KW complement system; Fc gamma receptor; cytotoxic effector cell;
KW host immune cell; programmed cell death; allergic disorder; cancer;
KW autoimmune disease; allergic asthma; atopic dermatitis; Crohn's disease;
KW allergic bronchopulmonary aspergillosis; allergic rhinitis;
KW Graves's disease; food allergy; allergic contact dermatitis; cancer;
KW B-cell lymphoma; rheumatoid arthritis; ulcerative colitis; psoriasis;

KW pigeon breeder's disease; hepatitis; leprosy; Lyme disease;
 KW diabetes mellitus; candidiasis; aplastic anaemia.
 XX
 OS Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 XX
 XX Key Location/Qualifiers
 PH Peptide 1..19
 FT /note= "signal peptide"
 FT Protein 20..140
 FT /note= "murine anti-human CD20 heavy chain variable
 FT region"
 FT Protein 141..470
 FT /note= "human gamma 1 heavy chain constant region"
 XX
 PN WO200044788-A1.
 XX
 XX 03-AUG-2000.
 PD
 XX 28-JAN-2000; 2000WO-US01893.
 PF
 XX 28-JAN-1999; 99US-0238741.
 PR
 XX (IDEC-) IDEC PHARM CORP.
 PA
 XX
 PI Braslawsky GR, Hanna N, Hariharan K, Labarre MJ, Huynh TB;
 XX
 DR WPI; 2000-514811/46.
 DR N-PSDB; AAA63531.
 XX
 PT Genetically engineering immunoglobulin (Ig) G/IgG dimers for the
 PT treatment of cancers, allergic disorders and autoimmune conditions -
 XX
 PS Example 1; Fig 2A-C; 65pp; English.
 XX
 CC The present sequence represents a dimeric anti-CD20 light chain
 CC polypeptide. The dimeric immunoglobulin is used in the method of the
 CC invention. The specification describes a method for producing an
 CC immunoglobulin (Ig) G/IgG dimer. The method comprises genetically
 CC engineering a monoclonal antibody to introduce a cysteine molecule
 CC which inhibits formation of intramolecular disulphide bridges between
 CC sister heavy chains on the same antibody molecule. The dimer is a
 CC homodimer or heterodimer that is capable of activating components of the
 CC complement system, and has the ability to activate and kill cells via the
 CC complement cascade. The dimer is also capable of binding to Fc gamma
 CC receptors on cytotoxic effector cells and on host immune cells, and is
 CC capable of initiating programmed cell death. The IgG/IgG dimers may be
 CC used to treat allergic disorders, cancers and autoimmune diseases such
 CC as allergic asthma, allergic bronchopulmonary aspergillosis, allergic
 CC rhinitis, atopic dermatitis, Crohn's disease, Graves's disease, food
 CC allergies, allergic contact dermatitis, CLL cancers and/or B-cell
 CC lymphomas. They may also be used to treat a range of other diseases and
 CC disorders such as rheumatoid arthritis, ulcerative colitis, psoriasis,
 CC pigeon breeder's disease, hepatitis, leprosy, Lyme disease, diabetes
 CC mellitus, candidiasis and aplastic anaemia. They are also useful for
 CC inducing hyper-cross-linking of membrane antigens and for the
 CC preferential killing of selected cell populations.
 XX
 SQ Sequence 470 AA;

Query Match 90.9%; Score 2287; DB 21; Length 470;
 Best Local Similarity 91.1%; Pred. No. 7.5e-131;
 Matches 428; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 MCWSCIILFLVATATGVHSQVGVOLVSGAEVKPKGASVKSCKASGYFTTSYMWQVQKAP 60
 DB 1 MGWSLILFLVAVATVLSVQLQPGAEIVKPGASVKSCKASGYFTTSYMWQVQKAP 60

QY 61 GQGLEWGMGEIDPSDYNTYNNQKFKATLTVDTSSTAYMELSSLSRSEDYATYYCARNRD 120
 DB 61 GRLGLEWIGAIYNGDTSYNGKFKATLTADKSSSTAYMQLSSITSEDSAVYYCARSTY 120

QY 121 YSNMYEDYWGEGTLVTVSSASTKGPSVFLAPSSKSTSGTAAALCLVKDYFPEPVTVS 180
 DB 121 Y9GDWYINVG9GTTVTVSSAATKGPSVFLAPSSKSTSGGTAALCLVKDYFPEPVTVS 180
 QY 181 WNSGALTSVHTFPAYLQSSGLYSLSVVTVTPSSSLGTQTYICNVNHIKPSNTKVDKRVPEP 240
 DB 181 WNSGALTSVHTFPAYLQSSGLYSLSVVTVTPSSSLGTQTYICNVNHIKPSNTKVDKRVPEP 240
 QY 241 KSCDKTHTCCPPAPPELLGGPSVFLPPPKDKDTLMSRTPEVTCVVVDVSHEDPEVKFNW 300
 DB 241 KSCDKTHTCCPPAPPELLGGPSVFLPPPKDKDTLMSRTPEVTCVVVDVSHEDPEVKFNW 300
 QY 301 YVDGVEVHNAKTPREEQYNSTYRVYVSLTVLHODWLNKKEYCKVSNKALPAPIEKTIS 360
 DB 301 YVDGVEVHNAKTPREEQYNSTYRVYVSLTVLHODWLNKKEYCKVSNKALPAPIEKTIS 360
 QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV 420
 DB 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV 420
 QY 421 LQSDGSFFLYSKLTVDKSRWQQGNVSCFVSVMHEALHNHYTQKSLSLSPGK 470
 DB 421 LQSDGSFFLYSKLTVDKSRWQQGNVSCFVSVMHEALHNHYTQKSLSLSPGK 470

RESULT 14
 AAEE03755
 ID AAEE03755 standard; Protein; 466 AA.
 XX
 AC AAEE03755;
 XX
 DT 07-AUG-2001 (first entry)
 XX
 DE Chimeric 2403 IgG antibody heavy chain (5F2.4H4.1E3).
 XX
 KW Murine; prostate stem cell antigen; PSMA; cytostatic; gene therapy;
 KW glycoprotein; cancer; prostate; bladder; lung; tumour; Ab; antibody;
 KW human; immunoglobulin G; IgG; heavy chain region.
 XX
 OS Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 PH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= Signal_peptide
 FT Protein 20..466
 FT /label= Mature_IgG_antibody_heavy_chain
 FT Region 1..141
 FT /note= "Derived from mouse heavy chain variable
 FT region (VH)"
 FT Region 142..466
 FT /note= "Derived from human IgG heavy chain constant
 FT region"
 XX
 PN WO200140309-A2.
 XX
 XX 07-JUN-2001.
 PD
 XX
 XX 27-OCT-2000; 2000WO-US29603.
 XX
 PR 29-OCT-1999; 99US-0162558.
 PR 16-FEB-2000; 2000US-0184872.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Devaux B, Keller G, Koeppe H, Lasky LA;
 XX
 DR WPI; 2001-389954/41.
 XX
 PT Novel anti-prostate stem cell antigen (PSMA) antibody that internalizes
 PT on binding to PSMA on mammalian cell and inhibits growth of
 PT PSMA-expressing cancer cells in vivo, useful for killing
 PT PSMA-expressing cancer cells -

XX PS Claim 5; Fig 13; 112pp; English.

XX CC The present chimeric sequence is full length 2403 immunoglobulin G (IgG)

CC antibody heavy chain (5F2.4H4.1E3) derived from murine heavy chain

CC variable region (VL) and human IgG heavy chain constant region.

CC This antibody binds to prostate stem cell antigen (PSCA) which is a

CC single subunit glycoprotein that is expressed on the cell surface as a

CC glycosylphosphatidylinositol (GPI)-anchored protein. The present

CC invention relates to anti-PSCA antibody composition and methods of

CC killing PSCA-expressing cancer cells. PSCA is useful for inhibiting and

CC killing the growth of PSCA-expressing cancer cells such as prostate

CC cancer, bladder cancer or lung cancer cells. Humanised antibody

CC conjugated to a toxin or a radioactive isotope is used for killing the

CC cancer cells. PSCA is useful for specifically targeting PSCA-expressing

CC tumour cells in vivo and for inhibiting or killing these cells. The

CC antibodies are also useful for treating the above mentioned cancers and

CC for diagnosing and staging of PSCA-expressing cancer, for purification

CC or immunoprecipitation of PSCA from cells, and for detection and

CC quantitation of PSCA in vitro. PSCA DNA is also useful for treating

CC cancers by gene therapy techniques.

XX SQ Sequence 466 AA;

Query Match 90.7%; Score 2283; DB 22; Length 466;

Best Local Similarity 91.1%; Pred. No. 1.3e-130;

Matches 428; Conservative 17; Mismatches 21; Indels 4; Gaps 1;

QY 1 MGWSCIIILFLVATATGSHVQVQLVQSGAEVKKPGASVKVSCKASGYTFTSWMQWVKQAP 60

Db 1 mgwsciiilflvatatgshvqvlvqsgaevkpgasvkvsckasgytftswmlnwvkqr 60

QY 61 GQGLEWMEIDPDSYNYNOKFKGKATLTVDSTSTAYMELSLRSDTAVYICARNRD 120

Db 61 grglewgridpsdseihdydkfdkdtlvdksststaiqlsltsedsavyycaitgi 120

QY 121 YSNWNYFDWGEGLTVTVSSASTGKPSVFPLAPSKSTSGGTAALGCLVKDYFPEPVTVS 180

Db 121 yamay----wqggtsvtvssaktgtpsvfplapskstksggtaalgclvkdyfpepvts 176

QY 181 WNSGALTSGVHTFPVAVLQSSGLYSLSSVTVTPSSSLGTOTVTCNVNHHKPSNTKVDKRV 240

Db 177 wnsгалtsghvhtfpavlgsglyslssvstvtpssslgtqtyicnvnhkpsntkvdckvpe 236

QY 241 KSCDKHTCCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300

Db 237 kscdkhtccpcpapellggsplfppkpkdtlmisrtpevtcvvdvshedpevkfnw 296

QY 301 YVDGVEVHNATKPREQYNSTYRVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTIS 360

Db 297 yvdgvevhnatkpreeqynstyrsvsvltvlhqdwlngkeyckvsnkalpapiektis 356

QY 361 KAGQPREPOVYITLPPSREEMTKNOVSLTCLVKGFPYSDIAVEVESNGOPENNYKTTTPPV 420

Db 357 kagqprepqvyitlppsreemtknqvsltcclvkgfypsdiavevesngqpennykttppv 416

QY 421 LDSGSEFLYSKLTVDKSRWQGVNFVSCVMHEALHNHYTQKSLSLSPGK 470

Db 417 ldsagsfllyskltvdksrwqgvnfvscvmhealhnhytqkslsislpkg 466

RESULT 15

AAB72232

ID AAB72232 standard; Protein; 464 AA.

XX AC AAB72232;

XX AC AAB72232;

XX AC AAB72232;

DT 10-MAY-2001 (first entry)

XX Humanised 323/A3 (IgG1) antibody heavy chain amino acid sequence.

XX Anti-Ep-CAM antibody; cyclic adenosine monophosphate; cell synthesis;

KW chemotherapeutic agent; cytostatic; anti-cancer therapy; cancer;

XX heavy chain.

OS Mus sp.

OS Homo sapiens.

PN WO200107082-A1.

XX 01-FEB-2001.

XX 23-JUL-1999; 99WO-EP05271.

XX 23-JUL-1999; 99WO-EP05271.

XX (GLAX) GLAXO GROUP LTD.

XX Knick VC, Stimmel JB, Thurmond LM;

XX WPI; 2001-182729/18.

PT Combination for treating cancer (e.g. breast, gastric or prostate

PT cancers), or in the manufacture of a medicament for anti-cancer

PT therapy, comprises an anti-Ep-cyclic adenosine monophosphate antibody

PT with a chemotherapeutic agent -

XX Example 3; Fig 7; 103pp; English.

XX This invention relates to a combination of an anti-Ep-CAM (cyclic

CC adenosine monophosphate) antibody with a chemotherapeutic agent, that is

CC capable of arresting Ep-CAM antigen expressing cells in the synthesis (S)

CC phase or the second growth phase (M) of cell enlargement (G2)/DNA

CC replication. The antibody exhibits cytostatic activity and is useful in

CC the manufacture of a medicament for use in anti-cancer therapy.

CC characterised in that a chemotherapeutic agent, which is capable of

CC arresting Ep-CAM antigen expressing cells in S or in G2/M, is

CC co-administered to a patient with an anti-Ep-CAM antibody. The

CC combination is useful for treating cancer, particularly colorectal

CC cancer, breast cancer, gastric cancer, prostate cancer or non-small-cell

CC lung cancer. The present sequence represents the heavy chain of

CC anti-Ep-CAM antibody known as humanised 323/A3 (IgG1) which can be

CC used in the combination of the invention.

XX SQ Sequence 464 AA;

Query Match 90.7%; Score 2282.5; DB 22; Length 464;

Best Local Similarity 91.7%; Pred. No. 1.4e-130;

Matches 430; Conservative 14; Mismatches 20; Indels 5; Gaps 2;

QY 1 MGWSCIIILFLVATATGSHVQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMOWVKQAP 60

Db 1 mgwsciiilflvatatgshvqvlvqsgaevkpgasvkvsckasgytftnygmwvrcap 60

QY 61 GQGLEWMEIDPDSYNYNOKFKGKATLTVDSTSTAYMELSLRSDTAVYICARNRD 120

Db 61 gqglewmgidpsdysnyynokfkgkatltvdststaymelslrsdtavyfcar--- 117

QY 121 YSNWNYFDWGEGLTVTVSSASTGKPSVFPLAPSKSTSGGTAALGCLVKDYFPEPVTVS 180

Db 118 fgn--yvdvgwqgslvtvssastgkpsvfplapskstksggtaalgclvkdyfpepvts 175

QY 181 WNSGALTSGVHTFPVAVLQSSGLYSLSSVTVTPSSSLGTOTVTCNVNHHKPSNTKVDKRV 240

Db 176 wnsгалtsghvhtfpavlgsglyslssvstvtpssslgtqtyicnvnhkpsntkvdckvpe 235

QY 241 KSCDKHTCCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300

Db 236 kscdkhtccpcpapellggsplfppkpkdtlmisrtpevtcvvdvshedpevkfnw 295

QY 301 YVDGVEVHNATKPREQYNSTYRVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTIS 360

Db 296 yvdgvevhnatkpreeqynstyrsvsvltvlhqdwlngkeyckvsnkalpapiektis 355

QY 361 KAKGPREPOVYTLPPSREMTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPV 420
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
356 kakgprepqvylppsrdeitknqvsitcivkgfypsdiawesngqpennyktppv 415
QY 421 LDSGSEFFLYSKLTYDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPG 469
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
416 ldsdgsfflyskltvdkrwrqgnvfscvmhealhnhytqkslsispg 464

Search completed: April 17, 2002, 16:38:55
Job time: 148 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 17, 2002, 16:39:21 ; Search time 21.24 Seconds
(without alignments)
497.954 Million cell updates/sec

Title: US-09-499-662-117
Perfect score: 2517
Sequence: 1 MWSCILFLVATATGVHSQ.....MHEALHNYTQKSLSPGK 470

Scoring table: BLOSOM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCPUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2229	88.6	449	1	US-08-458-516-13
2	2227	88.5	476	2	US-08-378-939-10
3	2199.5	87.4	467	4	US-09-049-672A-8
4	2197.5	87.3	452	3	US-09-027-449-71
5	2197.5	87.3	452	4	US-09-026-985-71
6	2161.5	85.9	454	2	US-07-934-373C-22
7	2161.5	85.9	454	3	US-08-437-642B-22
8	2161.5	85.9	454	5	PCT-US93-07832-22
9	2121	84.3	451	2	US-08-887-352B-14
10	2121	84.3	451	2	US-08-887-352B-16
11	2121	84.3	451	3	US-08-466-151-65
12	2121	84.3	451	4	US-09-109-207C-14
13	2121	84.3	451	4	US-09-109-207C-16
14	2121	84.3	451	4	US-09-296-005-16
15	2121	84.3	451	4	US-09-296-005-16
16	2118	84.1	478	3	US-08-487-550-8
17	2113	83.9	451	2	US-08-887-352B-18
18	2113	83.9	451	4	US-09-109-207C-18
19	2113	83.9	451	4	US-09-282-505-2
20	2113	83.9	451	4	US-09-054-255-2
21	2113	83.9	451	4	US-09-296-005-18
22	2102	83.5	453	3	US-08-466-151-8
23	2100.5	83.5	467	2	US-07-916-098A-45
24	2096.5	83.3	552	5	PCT-US93-07832-23
25	2093.5	83.2	469	2	US-07-934-373C-23
26	2093.5	83.2	469	3	US-08-437-642B-23
27	2087.5	82.9	459	1	US-08-157-101A-7

28 2069.5 82.2 467 1 US-08-704-744-81 Sequence 81, Appl
29 2067.5 82.1 473 4 US-09-049-672A-4 Sequence 4, Appl
30 2060.5 81.9 445 4 US-08-341-560B-17 Sequence 17, Appl
31 2054 81.6 476 3 US-08-487-550-12 Sequence 12, Appl
32 2051.5 81.5 446 3 US-08-397-411-7 Sequence 7, Appl
33 2022 80.3 476 3 US-08-487-550-4 Sequence 4, Appl
34 2019 80.2 442 5 PCT-US96-10043-9 Sequence 9, Appl
35 2007 79.7 442 1 US-08-461-968A-5 Sequence 5, Appl
36 2007 79.7 442 2 US-08-462-571-5 Sequence 5, Appl
37 1992.5 79.2 450 2 US-08-788-800-12 Sequence 12, Appl
38 1983 78.8 442 1 US-08-480-036-2 Sequence 2, Appl
39 1983 78.8 442 1 US-08-461-968A-2 Sequence 2, Appl
40 1983 78.8 442 2 US-08-462-571-2 Sequence 2, Appl
41 1983 78.8 442 5 PCT-US96-10043-12 Sequence 12, Appl
42 1945 77.3 443 5 PCT-US96-13152-4 Sequence 4, Appl
43 1875.5 74.5 467 4 US-08-523-894-12 Sequence 12, Appl
44 1874.5 74.5 467 4 US-08-523-894-8 Sequence 8, Appl
45 1867.5 74.2 467 4 US-08-523-894-10 Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-458-516-13
; Sequence 13, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-458-516-13

Query Match 88.6%; Score 2229; DB 1; Length 449;
Best Local Similarity 92.9%; Pred. No. 8.4e-160;
Matches 419; Conservative 15; Mismatches 15; Indels 2; Gaps 2;

QY 20 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYWQWVKQAPQGQLEWMEGIDPDSSTNY 79
Db 1 QVQLVQSGAEVKKPGSSVKVSKASGYFTSYLIEWVKQAPQGQLEWIGVYPGSGGTNY 60
QY 80 NQKFKGKATLVDTSTAYMELSSLSRSEDPAVYVCARNRDYSNNWYFDVWGEGLTVTS 139
Db 61 NEKFKGRVTLVDSTWYAYMELSSLSRSEDPAVYFCAR-RDNGYWG-FAYWQGTGLTVTS 118
QY 140 SASTKGPSVFLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLQS 199
Db 119 SASTKGPSVFLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLQS 178
QY 200 SGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRVKPKCDKTHCCPCPAPELLG 259
Db 179 SGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRVKPKCDKTHCCPCPAPELLG 238
QY 260 GPSVLEFPKPKDLMISRTPETVTVVVDVSHEDPEVKFNWYDGVVEVHNKTKPREEQY 319
Db 239 GPSVLEFPKPKDLMISRTPETVTVVVDVSHEDPEVKFNWYDGVVEVHNKTKPREEQY 298
QY 320 NSTYRVVSVTLVHLDWLNKGEYKCKVSKNKPALPAIEKTIKSKAKGQPREPOVYTLPPSRE 379
Db 299 NSTYRVVSVTLVHLDWLNKGEYKCKVSKNKPALPAIEKTIKSKAKGQPREPOVYTLPPSRE 358
QY 380 EMTKNQVSLCLVKGFYPSDIAVWESNGOPENNYKTPPVLDSDGSFFLYSKLTVDKSR 439
Db 359 ELTRNQVSLCLVKGFYPSDIAVWESNGOPENNYKTPPVLDSDGSFFLYSKLTVDKSR 418
QY 440 WQGNVFCSCVMHEALHNHYTKQSLSPGK 470
Db 419 WQGNVFCSCVMHEALHNHYTKQSLSPGK 449

RESULT 2

US-08-378-939-10
; Sequence 10, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:
; APPLICANT: CROME, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952640
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-378-939-10

Query Match 88.58; Score 2227; DB 2; Length 476;
Best Local Similarity 88.28; Pred. No. 1.3e-159;
Matches 420; Conservative 22; Mismatches 28; Indels 6; Gaps 1;

QY 1 MGWSCIIILFLVATATGHSOVQLVQSGAEVKKPGASVKVSKASGYTFTSYWQWVKQAP 60
Db 1 MDWTRELFVVAAATGVQSQMVQVQSGAEVKKPGSSVTVVSCASGGTFSNVAISWVRQAP 60
QY 61 GQGLEWMEGIDPDSSTNYNOKFKGKATLVDTSTAYMELSSLSRSEDPAVYVCARNR- 119
Db 61 GQGLEWMEGIIIFGTPTYSQNFQGRVITADKSTSTAHMELTSLRSEDPAVYVCATDRY 120
QY 120 -----DYSNNWYFDVWGEGLTVVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFP 174
Db 121 RQANFDRARVGVFPWQGTGLTVVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFP 180
QY 175 EPVTVSWNSGALTSGVHTTTPAVLOSGLYSLSSVTVVPSLSLGTQTYICNVNHNKPSNTKV 234
Db 181 EPVTVSWNSGALTSGVHTTTPAVLOSGLYSLSSVTVVPSLSLGTQTYICNVNHNKPSNTKV 240
QY 235 DKRVEPKSCDKTHCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP 294
Db 241 DKRVEPKSCDKTHCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP 300
QY 295 EVKFNWYDGVVEVHNKTKPREEQYNSTYRVVSVTLVHLDWLNKGEYKCKVSKNKPALPAP 354
Db 301 EVKFNWYDGVVEVHNKTKPREEQYNSTYRVVSVTLVHLDWLNKGEYKCKVSKNKPALPAP 360
QY 355 IEKTIKSKAKGQPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVWESNGOPENNY 414
Db 361 IEKTIKSKAKGQPREPOVYTLPPSREDELTKNOVSLTCLVKGFYPSDIAVWESNGOPENNY 420
QY 415 KTTPEVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 470
Db 421 KTTPEVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 476

RESULT 3

US-09-049-672A-8
; Sequence 8, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:

QY 317 EOYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGPREPQVYTLPP 376
DB 301 EOYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGPREPQVYTLPP 360
QY 377 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNKTTPPVLDSDGSFFLYSKLTV 436
DB 361 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNKTTPPVLDSDGSFFLYSKLTV 420
QY 437 KSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
DB 421 KSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 454

RESULT 7

US-08-437-642B-22
; Sequence 22, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 454 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

US-08-437-642B-22
Query Match 85.9%; Score 2161.5; DB 3; Length 454;
Best Local Similarity 89.4%; Pred. No. 1e-154;
Matches 406; Conservative 17; Mismatches 28; Indels 3; Gaps 1;

QY 20 QVOLQSGAEKVGKASVKSQSYFTTSYWMQVKAOPQGLWGEIDPDSYTN 79
DB 1 QVOLQSGPELVKPGASVKISCKTSGYFTTETMIMKQSHGKSLWIGGPNPKNGSSH 60

QY 80 NOKFKGKATLTVDTSITAYMELSLRSSEDTAVYYCARNRDYSNNW---YFDWMGEGTLY 136
DB 61 NOKRFDKATLAVDKSTSTAYMELSLTSDSGIYYCARWRGLNYGFDYRYFDWMGAGTTV 120
QY 137 TVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAV 196
DB 121 TVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAV 180
QY 197 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHCTCPCPAPE 256
DB 181 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHCTCPCPAPE 240
QY 257 LLGGPSVFLFPPKPKDRLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 316
DB 241 LLGGPSVFLFPPKPKDRLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 300
QY 317 EOYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGPREPQVYTLPP 376
DB 301 EOYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGPREPQVYTLPP 360
QY 377 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNKTTPPVLDSDGSFFLYSKLTV 436
DB 361 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNKTTPPVLDSDGSFFLYSKLTV 420
QY 437 KSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
DB 421 KSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 454

RESULT 8

PCT-US93-07832-22
; Sequence 22, Application PC/TUS9307832
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Immunglobulin Variants
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07832
; FILING DATE: 19930820
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 709P2PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 454 amino acids


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; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-887-352B-16

Query Match      84.3%; Score 2121; DB 2; Length 451;
Best Local Similarity 87.4%; Pred. No. 1.le-151;
Matches 395; Conservative 25; Mismatches 30; Indels 2; Gaps 2;

Qy 20 QVQLVQSGAEVKKPGASVKYSCKASGYTFTS-YMMQWVKQAPGGQLEWMGEIDPSDSTN 78
Db 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPGKLEWVASI-TYDGS 59

Qy 79 YNQKFKGKATLVDTSTAYMELSSLRSEDTAVYYCARNRDYNNWYFDVWGEGTLTV 138
Db 60 YNPVKGRITISRDDSKNTFYLMNSLRADTAIVYICARGSHYFGHWFHFAVWGQTLTV 119

Qy 139 SSASTKGPSVFPPLAPSSKSTSGGTAALGCLVDPPEVTVVSNWNGALTSVHTFPVAVLQ 198
Db 120 SSASTKGPSVFPPLAPSSKSTSGGTAALGCLVDPPEVTVVSNWNGALTSVHTFPVAVLQ 179

Qy 199 SSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRVKPKSCDKTHTCPCPAPELL 258
Db 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRVKPKSCDKTHTCPCPAPELL 239

Qy 259 GGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQ 318
Db 240 GGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQ 299

Qy 319 YNSTYRVVSVLTVLHQLDNLNGEKYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
Db 300 YNSTYRVVSVLTVLHQLDNLNGEKYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359

Qy 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKS 438
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKS 419

Qy 439 RWOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
Db 420 RWOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 11
US-08-466-151-65
; Sequence 65, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-Mar-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-Jan-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-May-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-Aug-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-466-151-65

Query Match      84.3%; Score 2121; DB 3; Length 451;
Best Local Similarity 87.4%; Pred. No. 1.le-151;
Matches 395; Conservative 25; Mismatches 30; Indels 2; Gaps 2;

Qy 20 QVQLVQSGAEVKKPGASVKYSCKASGYTFTS-YMMQWVKQAPGGQLEWMGEIDPSDSTN 78
Db 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPGKLEWVASI-TYDGS 59

Qy 79 YNQKFKGKATLVDTSTAYMELSSLRSEDTAVYYCARNRDYNNWYFDVWGEGTLTV 138
Db 60 YNPVKGRITISRDDSKNTFYLMNSLRADTAIVYICARGSHYFGHWFHFAVWGQTLTV 119

Qy 139 SSASTKGPSVFPPLAPSSKSTSGGTAALGCLVDPPEVTVVSNWNGALTSVHTFPVAVLQ 198
Db 120 SSASTKGPSVFPPLAPSSKSTSGGTAALGCLVDPPEVTVVSNWNGALTSVHTFPVAVLQ 179

Qy 199 SSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRVKPKSCDKTHTCPCPAPELL 258
Db 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRVKPKSCDKTHTCPCPAPELL 239

Qy 259 GGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQ 318
Db 240 GGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQ 299

Qy 319 YNSTYRVVSVLTVLHQLDNLNGEKYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
Db 300 YNSTYRVVSVLTVLHQLDNLNGEKYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359

Qy 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKS 438
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKS 419

Qy 439 RWOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
Db 420 RWOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 12
US-09-109-207C-14
; Sequence 14, Application us/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
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Db 1 EVQLVESGGGLVQPGGSLRLSCAVGSYITSGYSNHWIRQAQPGKLEWVASI-TYDGSIN 59
QY 79 YNQKFGKATLVTDVSTSTAYMELSLRSEDVAVYICARNRDYSNWYFDVWGEGTLTV 138
Db 60 YNPSVKGRITISRDDSKNTFYIQMNSLRAEDTAVYICARGSHYFGHWHFAVWGQGTFLTV 119
QY 139 SSASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSVGHVTPAVLIQ 198
Db 120 SSASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSVGHVTPAVLIQ 179
QY 199 SSGLYSLSSVTVTPSSSLGTQYIICNVNHPKNTKVDKRVKPKSCDKTHTCPCPAPELL 258
Db 180 SSGLYSLSSVTVTPSSSLGTQYIICNVNHPKNTKVDKRVKPKSCDKTHTCPCPAPELL 239
QY 259 GGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNNAKTKPREQ 318
Db 240 GGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNNAKTKPREQ 299
QY 319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSR 378
Db 300 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSR 359
QY 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFELYSKLTVDKS 438
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFELYSKLTVDKS 419
QY 439 RWOQGNVFSCSYNHEALHNHYTQKSLSLSPGK 470
Db 420 RWOQGNVFSCSYNHEALHNHYTQKSLSLSPGK 451
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RESULT 15

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US-09-296-005-16
; Sequence 16, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-Ige Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 16
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-296-005-16
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Query Match 84.3%; Score 2121; DB 4; Length 451;
Best Local Similarity 87.4%; Pred. NO. 1.1e-151;
Matches 395; Conservative 25; Mismatches 30; Indels 2; Gaps 2;

```
QY 20 OVQLVQSGAEVKKPGASVKCKASKGYFTS-YWQWVKQAQPGQGLEWNGEIDPSDSYTN 78
Db 1 EVQLVESGGGLVQPGGSLRLSCAVGSYITSGYSNHWIRQAQPGKLEWVASI-TYDGSIN 59
QY 79 YNQKFGKATLVTDVSTSTAYMELSLRSEDVAVYICARNRDYSNWYFDVWGEGTLTV 138
Db 60 YNPSVKGRITISRDDSKNTFYIQMNSLRAEDTAVYICARGSHYFGHWHFAVWGQGTFLTV 119
QY 139 SSASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSVGHVTPAVLIQ 198
Db 120 SSASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSVGHVTPAVLIQ 179
QY 199 SSGLYSLSSVTVTPSSSLGTQYIICNVNHPKNTKVDKRVKPKSCDKTHTCPCPAPELL 258
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Db 180 SSGLYSLSSVTVTPSSSLGTQYIICNVNHPKNTKVDKRVKPKSCDKTHTCPCPAPELL 239
QY 259 GGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNNAKTKPREQ 318
Db 240 GGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNNAKTKPREQ 299
QY 319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSR 378
Db 300 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSR 359
QY 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFELYSKLTVDKS 438
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFELYSKLTVDKS 419
QY 439 RWOQGNVFSCSYNHEALHNHYTQKSLSLSPGK 470
Db 420 RWOQGNVFSCSYNHEALHNHYTQKSLSLSPGK 451
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Search completed: April 17, 2002, 16:39:22
Job time: 145 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 17, 2002, 16:39:53 ; Search time 25.85 Seconds
(without alignments)
1384.992 Million cell updates/sec

Title: US-09-499-662-117
Perfect score: 2517
Sequence: 1 MWSCILLELVAFATGVHSQ.....MHEALNHVYTKLSLSPOK 470

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1758	69.8	330	1 GHU	Ig gamma-1 chain C
2	1639.5	65.1	377	2 A23511	Ig gamma-3 chain C
3	1637.5	65.1	377	2 A60764	Ig gamma-3 chain C
4	1610.5	64.0	469	2 S37483	Ig gamma-2a chain C
5	1610	64.0	326	1 G2HU	Ig gamma-2 chain C
6	1599.5	63.5	327	1 G4HU	Ig gamma-4 chain C
7	1546	61.4	474	1 G2MS11	Ig gamma-2b chain C
8	1544	61.3	446	2 S40295	Ig gamma-2a chain C
9	1501.5	59.7	475	2 S01321	Ig gamma-2b chain C
10	1471	58.4	470	2 S22080	Ig heavy chain pre
11	1467	58.3	472	2 S31459	Ig gamma-1 chain -
12	1432.5	56.9	444	2 PC4436	monoclonal antibod
13	1429	56.8	374	2 S69339	Ig heavy chain V r
14	1267	50.3	328	2 I47159	Ig gamma 2a chain
15	1261	50.1	328	2 I47160	Ig gamma 2b chain
16	1253	49.8	255	4 S31866	Ig gamma-1 chain C
17	1245	49.5	234	2 PT0207	Ig gamma chain C r
18	1235	49.1	328	2 I47158	Ig gamma 1 chain C
19	1231.5	48.9	323	1 GHRB	Ig gamma chain C r
20	1231	48.9	328	2 I47161	Ig gamma 3 chain C
21	1210.5	48.1	329	1 G2GP	Ig gamma-2 chain C
22	1165.5	46.3	308	2 C30554	Ig heavy chain C r
23	1157	46.0	289	1 G3HUW1	Ig gamma-3 heavy C
24	1155	45.9	326	2 PS0017	Ig gamma-1 chain C
25	1150	45.7	329	1 G3MSC	Ig gamma-3 chain C
26	1145	45.5	324	1 G1MS	Ig gamma-1 chain C
27	1144.5	45.5	333	2 PS0018	Ig gamma-2b chain C
28	1140	45.3	393	1 G1MSM	Ig gamma-1 chain C
29	1139	45.3	398	1 G3MSM	Ig gamma-3 chain C

30 1129 44.9 330 1 G2MSA
31 1127.5 44.8 329 2 S00847
32 1126.5 44.8 335 1 G2MSAB
33 1124 44.7 399 1 G2MSAM
34 1115 44.3 322 2 PS0019
35 1093.5 43.4 327 2 S06611
36 1080 42.9 405 1 G2MSBM
37 1070 42.5 277 2 I47162
38 993 39.5 548 2 S38864
39 940 37.3 627 2 S14683
40 922.5 36.7 549 2 S04845
41 864.5 34.3 241 2 S69131
42 851 33.8 246 2 S38950
43 795 31.6 220 2 A49444
44 759.5 30.2 249 2 S69340
45 759.5 30.2 572 2 B46529

ALIGNMENTS

RESULT 1

GHU

Ig gamma-1 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999

C;Accession: A93433; S3887; B90563; A90564; B91668; A91723; A02146

R;Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A;Reference number: A93433; MUID:82274238

A;Accession: A93433

A;Molecule type: DNA

A;Residues: 1-330 <ELL>

A;Cross-references: EMBL:Z17370

A;Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) marker

A;Note: Lys-330 is removed after translation

R;Harris, L.J.

submitted to the EMBL Data Library, October 1992

A;Reference number: S33904

A;Accession: S36861

A;Molecule type: DNA

A;Residues: 2-330 <HAR>

A;Cross-references: EMBL:Z17370

R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaudo, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of

A;Reference number: S33887; MUID:83001943

A;Accession: S33887

A;Molecule type: DNA

A;Residues: 88-113;235-330 <TAK>

A;Cross-references: EMBL:Z17370

R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman

Biochemistry 9, 3161-3170, 1970

A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq

A;Reference number: A90563; MUID:71064024

A;Contents: myeloma protein Eu

A;Accession: B90563

A;Molecule type: protein

A;Residues: 1-96,'R',98-135 <CUN>

A;Note: this sequence has the G1m(3) marker, 97-Arg

R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se

A;Reference number: A90564; MUID:71064025

A;Contents: Eu

A;Accession: A90564

A;Molecule type: protein

A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',2

A;Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met

R;Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A;Title: Die Primerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Ni

Igen Primaerstruktur.

A:Reference number: A91668; MUID:77070269
A:Contents: myeloma protein Nie
A:Accession: B91668
A:Molecule type: protein
A:Residues: 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C:Keywords: immunoglobulin

F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 65.18; Score 1637.5; DB 2; Length 377;
Best Local Similarity 82.88; Pred. No. 3.3e-86;
Matches 312; Conservative 7; Mismatches 11; Indels 47; Gaps 1;

QY 141 ASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPPTVTSWNSGALTSGVHTFPAVLQSS 200
DB 1 ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPPTVTSWNSGALTSGVHTFPAVLQSS 60
QY 201 GLYSSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRV----- 238
DB 61 GLYSSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRVELKTPLDGTHTCPCPCPEPKSC 120
QY 239 -----EPKSKDTHTCPCPCPEPKSCDTPPCPAPPELLGGPSVFLFPKPKDT 273
DB 121 DTPPCPCPCPEPKSCDTPPCPAPPELLGGPSVFLFPKPKDT 180
QY 274 LMISRTPEVTCVVDVSHEDPEVFNKTVYDGVVEVHNATKPREQYNSTYRVVSVLTVLH 333
DB 181 LMISRTPEVTCVVDVSHEDPEVFNKTVYDGVVEVHNATKPREQYNSTYRVVSVLTVLH 240
QY 334 QDWLNGKEYCKVSNKALPAPIETKISKAKGPREPQVYITLPPSREEMTKNQVSLTCLVK 393
DB 241 QDWLNGKEYCKVSNKALPAPIETKISKAKGPREPQVYITLPPSREEMTKNQVSLTCLVK 300
QY 394 GFYPDSIAVESNGQPNNTKTPPPVLDSDGSFFLYSKLTVDKSRMQGNVFCVSMHE 453
DB 301 GFYPDSIAVESNGQPNNTKTPPPVLDSDGSFFLYSKLTVDKSRMQGNVFCVSMHE 360
QY 454 ALHNHYTQKSLSLSPGK 470
DB 361 ALHNHYTQKSLSLSPGK 377

RESULT 4

Ig gamma-2a chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37483
R:Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A:Reference number: S37483
A:Accession: S37483
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-469 <DUC>
A:Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:276-345/Domain: immunoglobulin homology <IMM>

Query Match 64.08; Score 1610.5; DB 2; Length 469;
Best Local Similarity 64.48; Pred. No. 1.4e-84;
Matches 304; Conservative 60; Mismatches 103; Indels 5; Gaps 4;

QY 1 MGWSCIIFLVATATGVISQVQLVQSGAEVKKPGASVKASCKASGYTFTSYMMQWVKAP 60
DB 1 MGWSEWIFLLSGTAGVHCQIQQQSGPELVKPGASVKASCKASGYTFTSYMMQWVKAP 60
QY 61 GQGLWMEIDPDSYTYNKNFKGKATLVDITSTAYMELSSLRSDTAVYICARNRD 120
DB 61 GQGLWKWIIYIPASGNTKYNEFKGKATLVDITSSSTAYMQLSSLTSEDYVFCARAWG 120
QY 121 YSNKNYFDVWEGTLTVTSASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPPTVTS 180
DB 121 -ATATFLDYWGQGTTLTVTSASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPPTVTS 179
QY 181 WNSGALTSGVHTFPAVLQSSGLYSSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRV 240

DB 180 WNSGSLSGVHTFPAVLQSD-LYTLSSSVTVTSSTWPSQSTCNVAHPASSTKVDKKIEP 238
QY 241 KSCDKTHTCPP--CPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 298
DB 239 RG-PTIKPCPCPCPCAPNLLGGPSVFIKPKIKDVLMSLSPIVTCVVDVSEDDPDVQI 297
QY 299 NWYDGVVEVHNATKPREQYNSTYRVVSVLTVLHODWLNKEYCKVSNKALPAPIETK 358
DB 298 SWFNWVVEVHTAQTQTHREDYNTSLRVVSALPQIQHDMSCKEFKCKVNNKDLPIET 357
QY 359 ISKAKGPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVESNGQPNNTKTP 418
DB 358 ISKPKGSVRAQVYVLPPEPEEMTKQVLTLCWTDWDFPEDIYVETWNGKTELKNTPE 417
QY 419 PVLDSDGSFFLYSKLTVDKSRMQGNVFCVSMHEALHNHYTQKSLSLSPGK 470
DB 418 PVLDSDGSFYFYSKLRVEKKNWERNYSYCSVVEGLHNHHTKTSFSRTPGK 469

RESULT 5

G2HU
Ig gamma-2 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C:Accession: A93906; A92809; A90752; A93132; A02148
R:Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain
A:Reference number: A93906; MUID:82197621
A:Accession: A93906
A:Molecule type: DNA
A:Residues: 1-326 <ELL>
A:Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056
A:Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, an
A:Reference number: A92809; MUID:81007873
A:Contents: myeloma protein Til
A:Accession: A92809
A:Molecule type: protein
A:Residues: 1-19 'Q', 21-57 'Z', 59 'A', 61-193 'D', 195-325 <WAN>
A:Note: Trp 156 is at or near the complement-binding site
R:Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A:Title: The amino acid sequences of the three heavy chain constant region domains of
A:Reference number: A90752; MUID:80001357
A:Contents: myeloma protein Zie
A:Accession: A90752
A:Molecule type: protein
A:Residues: 1-24 'E', 26-57 'EV', 60-85; 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 1
A:Note: this sequence has since been revised
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin
A:Reference number: A93132; MUID:80114419
A:Contents: Zie
A:Accession: A93132
A:Molecule type: protein
A:Residues: 238-275 <HOF>
R:Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A:Reference number: A94591
A:Contents: annotation; Zie
A:Note: the revised sequence differs from that shown in having 60-Ala and in the amid
ned
R:Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A:Reference number: A90253; MUID:72033500
A:Contents: annotation; myeloma protein Sa, disulfide bonds
R:Frangione, B.; Milstein, C.; Pink, J.R.L.

Nature 221, 145-148, 1969
A:Title: Structural studies of immunoglobulin G.
A:Reference number: A93157; MUID:69064124
A:Contents: annotation; Sa, disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG2
A:Cross-references: GDB:119338; OMIM:147110
A:Map position: 14q32.33-14q32.33
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:133-202/Domain: immunoglobulin homology <IM2>
F:239-306/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: Interchain (to light chain) #status experimental
F:27-83,140-200,246-304/Disulfide bonds: Interchain (to heavy chain) #status experimental
F:102,103,106,109/Disulfide bonds: Interchain (to heavy chain) #status experimental
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 64.0%; Score 1610; DB 1; Length 326;
Best Local Similarity 91.8%; Pred. No. 1e-84;
Matches 303; Conservative 10; Mismatches 13; Indels 4; Gaps 2;

QY 141 ASTKGPSVFLPAPSSKSTSGTAAALGCLVDYPPPEVTVSWNSGALTSGVHTFPVAVLQSS 200
Db 1 ASTKGPSVFLPAPSSKSTSGTAAALGCLVDYPPPEVTVSWNSGALTSGVHTFPVAVLQSS 60

QY 201 GLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKVDKRVKPKSCDKTHTCPPCAPELLGG 260
Db 61 GLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKVDKRVKPKSCDKTHTCPPCAPELLGG 116

QY 261 PSVFLPPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNKTKPREQYN 320
Db 117 PSVFLPPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNKTKPREQYN 176

QY 321 STYRVVSLVTLVHODWLNGLNGKEYCKVSNKALPAPIETKISKAKGQPREPOVYTLPPSREE 380
Db 177 STYRVVSLVTLVHODWLNGLNGKEYCKVSNKALPAPIETKISKAKGQPREPOVYTLPPSREE 236

QY 381 MTKNQVSLTCLVGFPSDIAVWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 440
Db 237 MTKNQVSLTCLVGFPSDIAVWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 296

QY 441 QQGNVFCSCVHHEALHNHYTQKSLSLSPGK 470
Db 297 QQGNVFCSCVHHEALHNHYTQKSLSLSPGK 326

RESULT 6
G4HU
Ig gamma-4 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C:Accession: A90933; A90249; A02150
R:Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A:Reference number: A90933; MUID:83157104
A:Accession: A90933
A:Molecule type: DNA
A:Residues: 1-327 <ELL>
A:Note: the sequence was determined from the germline gene
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant r
A:Reference number: A90249; MUID:70207560
A:Accession: A90249
A:Molecule type: protein
A:Residues: 1-30;81-326 <PIN>
C:Genetics:
A:Gene: GDB:IGHG4

A:Cross-references: GDB:119340; OMIM:147130
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 111/1; 221/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k) hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:134-203/Domain: immunoglobulin homology <IM2>
F:240-307/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: Interchain (to light chain) #status experimental
F:27-83,141-201,247-305/Disulfide bonds: Interchain (to heavy chain) #status predicted
F:106,109/Disulfide bonds: Interchain (to heavy chain) #status experimental
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 63.5%; Score 1599.5; DB 1; Length 327;
Best Local Similarity 91.8%; Pred. No. 4e-84;
Matches 303; Conservative 9; Mismatches 15; Indels 3; Gaps 1;

QY 141 ASTKGPSVFLPAPSSKSTSGTAAALGCLVDYPPPEVTVSWNSGALTSGVHTFPVAVLQSS 200
Db 1 ASTKGPSVFLPAPSSKSTSGTAAALGCLVDYPPPEVTVSWNSGALTSGVHTFPVAVLQSS 60

QY 201 GLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKVDKRVKPKSCDKTHTCPPCAPELLGG 260
Db 61 GLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKVDKRVKPKSCDKTHTCPPCAPELLGG 117

QY 261 PSVFLPPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNKTKPREQYN 320
Db 118 PSVFLPPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNKTKPREQYN 177

QY 321 STYRVVSLVTLVHODWLNGLNGKEYCKVSNKALPAPIETKISKAKGQPREPOVYTLPPSREE 380
Db 178 STYRVVSLVTLVHODWLNGLNGKEYCKVSNKALPAPIETKISKAKGQPREPOVYTLPPSREE 237

QY 381 MTKNQVSLTCLVGFPSDIAVWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 440
Db 238 MTKNQVSLTCLVGFPSDIAVWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 297

QY 441 QQGNVFCSCVHHEALHNHYTQKSLSLSPGK 470
Db 298 QQGNVFCSCVHHEALHNHYTQKSLSLSPGK 327

RESULT 7
C2MS11
Ig gamma-2b chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C:Accession: S25057; A02157; A26235; A26233; A53598
R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specifi
A:Reference number: S25057
A:Accession: S25057
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-474 <FIS>
A:Cross-references: EMBL:X67210; NID:g54826; PIDN:CAA47649.1; PID:g54827
R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned fro
A:Reference number: A02157; MUID:80120716
A:Contents: a allele
A:Accession: A02157
A:Molecule type: DNA
A:Residues: 138-161, 'L', 163-189, 'Fp', 193-474 <YAM>
A:Cross-references: GB:J00461
A:Note: the sequence was determined from the germline gene
R:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
Science 206, 1299-1303, 1979

Db 355 EEEMTKQVILTCMTDFMPEDIVVETNNGKTELNTKTEPVLDSGSPFMSKLRVEK 414
Qy 438 SRWQGNVFCSCVMHEALHNHYTKQSLSPG 469
Db 415 KNWVERNSYSCSVVHEGLHNHHTTKSPSRTPG 446

RESULT 9
S01321
Ig gamma-2b chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C:Accession: S01321
R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed a
A:Reference number: S01320; MUID:88329081
A:Accession: S01321
A:Molecule type: mRNA
A:Residues: 1-475
A:Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781
A:Note: this sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>
F:159-223/Domain: immunoglobulin homology <IMM>

Query Match 59.7%; Score 1501.5; DB 2; Length 475;
Best Local Similarity 60.6%; Pred. No. 2.3e-78;
Matches 289; Conservative 66; Mismatches 113; Indels 9; Gaps 4;

Qy 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKPGASVKVKASGYTFTSYMMQWVKQAP 60
Db 1 MEWITWFLFILSGTAGVQSQVQLQSGAEIARPGASVKLSCKASGYTLTIGISWVKQT 60
Qy 61 GQLEWMEIDPSDSTYNNQKFKGKATLVDTSTAYMELSSLRSEDTAVTYICARNRD 120
Db 61 GQLEWIGETIYPGSGNSYFNEKEFKGKATLVDKSSSTAYLHLSSLTSDSAVYFCAGPRQ 120
Qy 121 YSNWVDFVWGEGLTVTSASATKGPSVFLPAPSSSTSGTAAALGCLVKDYPEPTVS 180
Db 121 V-GLLPFGYWGQGLTVTASAAKTPPSVPLAPGCGDTTGGSSVTLGCLVKGYFPESVTV 179
Qy 181 WNSGALTSGVHTTTPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKRVEP 240
Db 180 WNSGSLSSVHTTTPALLO-SGLYTMSSSVTVPSWTPSQVITCVSAHPASSTVDDKLEP 238
Qy 241 KSCDKT-HTC-----CPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHED 293
Db 239 SGTSTINPCPCKECHKCAPNLEGGPSVFIPPNKIDVLMISLTPKVTCTVVVDVSEDD 298
Qy 294 PEYKFNWYDGEVHNHAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 353
Db 299 PDVQISWNVNVEFLTAQTQTHREDYNSTIRVVSALPIQHDQWMSGEKFKCKVNNKDLPA 358
Qy 354 PIEKTIKAKGQPREQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENN 413
Db 359 PIERTISKIGIYRAQVYILSPPPQLSKRDKVSLTCLAVGFSPEDISVETWNGHTEEN 418
Qy 414 YKTPPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPG 470
Db 419 YKDTAPVLDSDGSFYIYKLNMTKSKWEKTDSPSCNVRHEGLKNLYLKKTISSPGK 475

RESULT 10
S22080
Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
N:Alternate names: Ig gamma-1 chain C region (clone 8.10)
C:Species: Bos primigenius taurus (cattle)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S22080; S06610; A31303
R:Sanders, P.G.
submitted to the EMBL Data Library, November 1991
A:Reference number: S22080
A:Accession: S22080
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-470 <SAN>
A:Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440
R:Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A:Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and g
A:Reference number: S06610; MUID:90097956
A:Accession: S06610
A:Molecule type: DNA
A:Residues: 142-470 <SYM>
A:Cross-references: EMBL:X16701
A:Note: the sequence was determined from the germline gene
C:Genetics:
A:Gene: Ig CH gamma-1
A:Introns: 98/1; 111/1; 221/1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F:161-225/Domain: immunoglobulin homology <IMM>
F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 58.4%; Score 1471; DB 2; Length 470;
Best Local Similarity 60.0%; Pred. No. 1.2e-76;
Matches 283; Conservative 64; Mismatches 115; Indels 10; Gaps 7;

Qy 3 WSCIILFLVATATGVHSQVQLVQSGAEVKPGASVKVKASGYTFTSYMMQWVKQAPGQ 62
Db 5 WT--LLFVLSAPIGVLSQVQLRESGSLVKPSQTLSTCTVSGFSLSYALTWVRQAPGK 62
Qy 63 GLEWMEIDPSDSTYNNQKFKGKATLVDTSTAYMELSSLRSEDTAVTYICARNR--D 120
Db 63 ALEWVGGI-TSGGTTYNNPALKSRLSITKENSQVSLSVSVTPEDTATYYCARSTYE 121
Qy 121 YSNWVDFVWGEGLTVTSASATKGPSVFLPAPSSSTSGTAAALGCLVKDYPEPTVS 180
Db 122 VGGATADAWGQGLTVTSASATPAKVPFLSSCCGDKSSSTVTLGCLVSSYMPPEPTVT 181
Qy 181 WNSGALTSGVHTTTPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKRVEP 240
Db 182 WNSGALKSGVHTTTPAVLQSSGLYSLSSVTVTPGSTG-QFTFCNVAPASSTKVDKAVDP 240
Qy 241 KSCDKTHTCPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFNW 300
Db 241 -TC-KPSPDCPCPPPELPGGPSVFIPPKPKDTLTISGTPETVTCVVVDVGDHDPPEVFSW 298
Qy 301 YVDGVEVHNHAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
Db 299 FVDDVEVNTATTPREEQFNSTYRVVSALRIQHDQWTCGKEFKCKVHNEGLPAIVRTIS 358
Qy 361 KAKGQPREQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVWESNGQP--ENNYKTP 418
Db 359 RTKGPAEPQVYVLAAPQEEELSKSTVSLTCMVTSTFYPDYIAVWENRQNGQPESEDKYGTTP 418
Qy 419 PVLDSGCSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 470
Db 419 PQLDADSSVFLYSLKLRVDRNSWQEGDTYTCVVMHEALHNHYTKQSTKSAGK 470

RESULT 11
S31459
Ig gamma-1 chain - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C:Accession: S31459
R:Patric, S.; Nau, F.
submitted to the EMBL Data Library, December 1992
A:Reference number: S31459


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QY 182 NSGALTSVHTFPAVLQSSGLYSLSSVTVPPSSSLGTGTQYICNVNHNKPSNTKVKDRVEPK 241
Db 143 -----EPK 145

QY 242 SCDKTHTCPCPAPPELLGGPSVFLPDKPTLMISRTPEVTCVVVDVSHEDPEVKFNWY 301
Db 146 SCDKTHTCPCPAPPELLGGPSVFLPDKPTLMISRTPEVTCVVVDVSHEDPEVKFNWY 205

QY 302 VDGVEVHNATKPREQYNSTYRVSVLTVLHODWLNKGEYCKVSNKALPAPIETKISK 361
Db 206 VDGVEVHNATKPREQYNSTYRVSVLTVLHODWLNKGEYCKVSNKALPAPIETKISK 265

QY 362 AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 421
Db 266 AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 325

QY 422 DSDGSFPLYSKLTVDKSRWQOGNVEFSCVMHEALHNHYTOKSLSPGK 470
Db 326 DSDGSFPLYSKLTVDKSRWQOGNVEFSCVMHEALHNHYTOKSLSPGK 374

RESULT 14
I47159
Ig gamma 2a chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47159
R:KacsKovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845
A:Accession: I47159
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
C:Genetics:
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: Immunoglobulin homology <IMM>

Query Match 50.3%; Score 1267; DB 2; Length 328;
Best Local Similarity 69.9%; Pred. No. 3.1e-65;
Matches 232; Conservative 42; Mismatches 52; Indels 6; Gaps 2;

QY 141 ASTKGPSVFLPAPSSKSTSGGTAAAGCLVKDYFPEPTVWNSGALTSVHTFPAVLQSS 200
Db 1 APTAPSVFLPAPCSRDTSGPNVALGLASSYFPEPTVWNSGALSSGVHTFPSVLQPS 60

QY 201 GLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVKDRVEPKSCDKTHTCPCPAPELLGG 260
Db 61 GLYSLSSMTVPASSLSKSYTCNVNHPATTTKDKRVGTKTKPPCPICPACESP----G 116

QY 261 PSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 320
Db 117 PSVFIPLPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHTAQRKEEQFN 176

QY 321 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSREE 380
Db 177 STYRVSVLTPLQHDWLNKGEYCKVSNKALPAPIETRIISKAKGQTPREPOVYTLPPHAE 236

QY 381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKS 438
Db 237 LSRKSVSITCLVIGFYPPDIDVEMQRNGQPEPEGNRTTTPPQQQVDGTYFLYKFSVDKA 296

QY 439 RWQOGNVEFSCVMHEALHNHYTOKSLSPGK 470
Db 297 SWQGGGIFQCAVMHEALHNHYTOKSISKTPGK 328

Search completed: April 17, 2002, 16:39:54
Job time: 167 sec
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RESULT 15
I47160

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OM protein - protein search, using sw model

Run on: April 17, 2002, 16:41:04 ; Search time 17.09 Seconds
(without alignments)
1008.336 Million cell updates/sec

Title: US-09-499-662-117

Perfect score: 2517

Sequence: 1 MGVSCILLFLVATATGVHQS.....MHEALNHVYTKSLSPCK 470

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1758	69.8	330	1 GCL_HUMAN	P01857 homo sapien
2	1610	64.0	326	1 GCL_HUMAN	P01859 homo sapien
3	1599.5	63.5	327	1 GC4_HUMAN	P01861 homo sapien
4	1231.5	48.9	323	1 GC_RABIT	P01870 oryctolagus
5	1210.5	48.1	329	1 GC2_CAVPO	P01862 cavia porce
6	1162	46.2	290	1 GC3_HUMAN	P01860 homo sapien
7	1155	45.9	326	1 GCL_RAT	P20759 rattus norv
8	1150	45.7	329	1 GC3_MOUSE	P22436 mus musculu
9	1145	45.5	324	1 GCL_MOUSE	P01868 mus musculu
10	1144.5	45.5	333	1 GCB_RAT	P20761 rattus norv
11	1140	45.3	333	1 GCL_MOUSE	P01869 mus musculu
12	1139	45.3	398	1 GC3_MOUSE	P03987 mus musculu
13	1129	44.9	330	1 GCAA_MOUSE	P01863 mus musculu
14	1127.5	44.8	329	1 GCC_RAT	P20762 rattus norv
15	1126.5	44.8	335	1 GCAB_MOUSE	P01864 mus musculu
16	1124	44.7	399	1 GCAM_MOUSE	P01865 mus musculu
17	1115	44.3	322	1 GCB_RAT	P20760 rattus norv
18	1085	43.1	336	1 GCB_MOUSE	P01866 mus musculu
19	1080	42.9	405	1 GCB_MOUSE	P01867 mus musculu
20	559.5	22.2	139	1 HV07_MOUSE	P01751 mus musculu
21	528	21.0	117	1 HV06_MOUSE	P01750 mus musculu
22	521.5	20.7	137	1 HV11_MOUSE	P01755 mus musculu
23	521	20.7	138	1 HV48_MOUSE	P03980 mus musculu
24	516	20.5	117	1 HV05_MOUSE	P01749 mus musculu
25	507	20.1	140	1 HV02_MOUSE	P01746 mus musculu
26	504	20.0	117	1 HV09_MOUSE	P01753 mus musculu
27	491	19.5	117	1 HV04_MOUSE	P01748 mus musculu
28	488	19.4	117	1 HV49_MOUSE	P06328 mus musculu
29	486.5	19.3	429	1 EPC_RAT	P01855 rattus norv
30	486	19.3	428	1 EPC_HUMAN	P01854 mus musculu
31	482	19.1	117	1 HV10_MOUSE	P01754 mus musculu
32	479	19.0	136	1 HV15_MOUSE	P01759 mus musculu
33	477	19.0	117	1 HV16_HUMAN	P23083 homo sapien

34	471	18.7	421	1 EPC_MOUSE	P06336 mus musculu
35	467	18.6	117	1 HV1B_HUMAN	P01743 homo sapien
36	460	18.3	117	1 HV12_MOUSE	P01756 mus musculu
37	459	18.2	117	1 HV13_MOUSE	P01757 mus musculu
38	457.5	18.2	147	1 HV1C_HUMAN	P01744 homo sapien
39	454.5	18.1	120	1 HV50_MOUSE	P06329 mus musculu
40	448	17.8	120	1 HV03_MOUSE	P01747 mus musculu
41	446.5	17.7	455	1 MUC_MOUSE	P01872 mus musculu
42	445	17.7	454	1 MUC_HUMAN	P01871 homo sapien
43	439	17.4	458	1 MUC_RABIT	P03988 oryctolagus
44	438	17.4	121	1 HV01_MOUSE	P01745 mus musculu
45	436.5	17.3	476	1 MUCM_MOUSE	P01873 mus musculu

ALIGNMENTS

RESULT 1					
1	GCL_HUMAN				
ID	GCL_HUMAN	STANDARD;	PRT;	330 AA.	
AC	P01857;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	IG GAMMA-1 CHAIN C REGION.				
GN	IGHG1.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.				
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RA	Ellison J.W., Berson B.J., Hood L.E.;				
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene."				
RL	Nucleic Acids Res. 10:4071-4079(1982).				
RN	[2]				
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RX	MEDLINE=71064024; PubMed=3489771;				
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,				
RA	Waxdal M.J., Edelman G.M.;				
RT	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino				
RL	acid sequence of heavy-chain cyanogen bromide fragments H1-H4."				
RN	Biochemistry 9:3161-3170(1970).				
[3]					
RP	SEQUENCE OF 136-329 (EU).				
RX	MEDLINE=71064025; PubMed=5530842;				
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,				
RA	Edelman G.M.;				
RT	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino				
RL	acid sequence of heavy-chain cyanogen bromide fragments H5-H7."				
RN	Biochemistry 9:3171-3181(1970).				
[4]					
RP	SEQUENCE (MYELOMA PROTEIN NIE).				
RX	MEDLINE=77070269; PubMed=826475;				
RA	Ponstingl H., Hilschmann N.;				
RT	"The rule of antibody structure. The primary structure of a				
RL	monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The				
RT	chymotryptic peptides of the H-chain, alignment of the tryptic				
RL	peptides and discussion of the complete structure."				
RN	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).				
[5]					
RP	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.				
RX	MEDLINE=83289131; PubMed=684994;				
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;				
RT	"Three-dimensional structure determination of antibodies. Primary				
RL	structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."				
RN	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).				
[6]					
RP	DISULFIDE BONDS.				
RX	MEDLINE=71064027; PubMed=4923144;				
RA	Gall W.E., Edelman G.M.;				
RT	"The covalent structure of a human gamma G-immunoglobulin. X.				

RT Intrachain disulfide bonds *;
 RL Biochemistry 9:3188-3196(1970).
 RN [7]
 RX DISULFIDE BONDS.
 RX MEDLINE=77070267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.:
 RA "Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
 RT characterization of the protein, the L- and H-chains, the
 RT cyanogen bromide cleavage products, and the disulfide bridges.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=81208100; PubMed=7236608;
 RA Deisenhofer J.;
 RA "Crystallographic refinement and atomic models of a human Fc fragment
 RT and its complex with fragment B of protein A from Staphylococcus
 RT aureus at 2.9- and 2.8-A resolution.";
 RL Biochemistry 20:2361-2370(1981).
 CC -1- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE
 CC GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3)
 CC MARKER & THE GIM (NON-1) MARKERS.
 CC -1- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
 CC 35,116,198,269 & 272.
 CC -1- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
 CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
 CC 268-272.
 CC -1- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
 CC RESIDUES 198,267&272.
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 CC -----
 DR EMBL; J00228; AAC82527.1; AUT_INIT.
 DR FIR; A02146; GHU.
 DR PDB; 1FC1; 15-JUL-92.
 DR PDB; 1FC2; 15-JUL-92.
 DR MIM; 147100; -
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_cl.
 DR InterPro: IPR003600; Ig_like.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00407; Igcl; 2.
 DR SMART; SM00410; Ig_like; 1.
 DR PROSITE; PS00290; Ig_MHC; 2.
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 3D-structure.
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 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 223 CH2.
 FT DOMAIN 224 330 CH3.
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 FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).
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 FT VARIANT 241 241
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 FT HELIX 130 134
 N-LINKED (GLCNAC...)
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 /FTId=VAR_003886.
 D -> E (IN GIM(NON-1) MARKER).
 /FTId=VAR_003887.
 L -> M (IN GIM(NON-1) MARKER).
 /FTId=VAR_003888.

FT	TURN	136	137
FT	STRAND	141	148
FT	STRAND	158	162
FT	TURN	163	164
FT	STRAND	165	166
FT	STRAND	175	178
FT	STRAND	183	190
FT	HELI	193	197
FT	TURN	198	199
FT	STRAND	202	206
FT	STRAND	215	219
FT	STRAND	227	227
FT	STRAND	230	234
FT	HELI	238	240
FT	TURN	241	242
FT	STRAND	245	256
FT	STRAND	260	266
FT	TURN	267	268
FT	STRAND	269	270
FT	STRAND	274	276
FT	STRAND	280	281
FT	TURN	283	284
FT	STRAND	287	296
FT	HELI	297	301
FT	TURN	302	303
FT	STRAND	306	312
FT	TURN	313	314
FT	TURN	316	317
FT	STRAND	320	324
SQ	SEQUENCE	330 AA; 36106 MW; 3770EE106C2FA33D CRC64;	

Query Match 69.8%; Score 1758; DB 1; Length 330;
 Best Local Similarity 99.1%; Pred. No. 9.9e-114;
 Matches 327; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY	141	ASTKGSVFPLAPSSKSTSGTAAALCLVKDYDPEPVTVSVNSGALTSGVHTPFAVLQSS	200
DB	1	ASTKGSVFPLAPSSKSTSGTAAALCLVKDYDPEPVTVSVNSGALTSGVHTPFAVLQSS	60
QY	201	GLYSLSSVTVPPSSSLGTQYICNVNHPKSTKVDKVEPKSCDKTHCTCPCPAPELGG	260
DB	61	GLYSLSSVTVPPSSSLGTQYICNVNHPKSTKVDKVEPKSCDKTHCTCPCPAPELGG	120
QY	261	PSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNHYVDGVEVHNNAKTPREQYN	320
DB	121	PSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNHYVDGVEVHNNAKTPREQYN	180
QY	321	STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE	380
DB	181	STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE	240
QY	381	MTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW	440
DB	241	LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW	300
QY	441	QQGNVFSCSVMHEALHNHYTQKSLSLSPGK	470
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 AC P01859;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
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 GN IGHG2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82197621; PubMed=6804948;
RA Ellison J.W., Hood L.E.;
RT "Linkage and sequence homology of two human immunoglobulin gamma
RL heavy chain constant region genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
RN [2]
RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX MEDLINE=81007873; PubMed=6774012;
RA Wang A.-C., Tung E., Fudenberg H.H.;
RT "The primary structure of a human IgG2 heavy chain: genetic,
RL evolutionary, and functional implications.";
RL J. Immunol. 125:1048-1054(1980).
RN [3]
RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
RX MEDLINE=80001357; PubMed=1113060;
RA Connell G.E., Parr D.M., Hofmann T.;
RT "The amino acid sequences of the three heavy chain constant region
RL domains of a human IgG2 myeloma protein.";
RL Can. J. Biochem. 57:758-767(1979).
RN [4]
RP SEQUENCE OF 238-275 (ZIE).
RX MEDLINE=80114419; PubMed=118920;
RA Hofmann T., Parr D.M.;
RT "A note of the amino acid sequence of residues 381-391 of human
RL immunoglobulins gamma chains.";
RL Mol. Immunol. 16:923-925(1979).
RN [5]
RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
RA Hofmann T., Parr D.M.;
RL Submitted (MAR-1980) to the PIR data bank.
RN [6]
RP SEQUENCE OF 1-121 (DOT).
RX MEDLINE=95255298; PubMed=7737190;
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT "Characterization of the two unique human anti-flavin monoclonal
RL immunoglobulins.";
RL Eur. J. Biochem. 228:886-893(1995).
RN [7]
RP DISULFIDE BONDS.
RX MEDLINE=72033500; PubMed=4940472;
RA Milstein C., Frangione B.;
RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
RL Biochem. J. 121:217-225(1971).
RN [8]
RP DISULFIDE BONDS.
RX MEDLINE=69064124; PubMed=5782707;
RA Frangione B., Milstein C., Pink J.R.L.;
RT "Structural studies of immunoglobulin G.";
RL Nature 221:145-148(1969).
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CC EMBL: V00554; CAB58438.1; -;
DR PIR: A02148; G2HU.
DR MIM: 147110; -;
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR003600; Ig-like.
DR Pfam: PF00047; Ig; 3.
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DR PROSITE: PS00290; IG_MHC; 2.
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RN NON_TER 1 1

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FT DOMAIN 111 219 CH2.
FT DOMAIN 220 326 CH3.
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FT DISULFID 27 83 INTERCHAIN (WITH A LIGHT CHAIN).
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FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 246 304
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SQ
Query Match 64.08; Score 1610; DB 1; Length 326;
Best Local Similarity 91.8%; Pred. No. 1.4e-103;
Matches 303; Conservative 10; Mismatches 13; Indels 4; Gaps 2;
QY 141 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
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DB 61 GLYSLSSVTVFSSSNFGTQTYICNVNHKPSNTKYVDKRVKPSCKDHTHTCPPCPAPELLGG 116
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ID GC4_HUMAN
AC P01861;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
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GN IGHG4.
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RN [1]
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RX MEDLINE=83157104; PubMed=6299662;
RA Ellison J.W., Buxbaum J.N., Hood L.E.;
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL DNA 1:11-18(1981).
RN [2]
RP SEQUENCE OF 1-30 AND 81-326.
RX MEDLINE=70207560; PubMed=4192699;
RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
RN constant region of a gamma 4 chain.";

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RL Biochem. J. 117:33-47(1970).
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DR EMBL; K01316; AAB59394.1; ALT_INIT.
DR PIR; A02150; G4HU.
DR MIM; 147130; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IgC1; 2.
DR SMART; SM00410; Ig_Like; 1.
DR PROSITE; PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 220 CH2.
FT DOMAIN 221 327 CH3.
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 83
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
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FT DISULFID 247 305
SQ SEQUENCE 327 AA; 35940 MW; 3E0BD811EF208E7A CRC64;

Query Match 63.5%; Score 1599.5; DB 1; Length 327;
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QY 201 GLYSLSVTVTPSSSLGTQTYICNVNHNKSNKTVKDRVPEKSCDKTHTCPCPAPELGG 260
Db 61 GLYSLSVTVTPSSSLGTQTYICNVNHNKSNKTVKDRVPEKSCDKTHTCPCPAPELGG 117

QY 261 PSVFLPFPKPKDLMISRPTEVTCVVVDVSHEDPEVKENNYVDGVVEVHNAKTPREEQYN 320
Db 118 PSVFLPFPKPKDLMISRPTEVTCVVVDVSHEDPEVKENNYVDGVVEVHNAKTPREEQYN 177

QY 321 STYRVSVSLTVLHQDLNGLKEYCKYKNKALPAPIETKISKAKGQPREPQVYTLPPSREE 380
Db 178 STYRVSVSLTVLHQDLNGLKEYCKYKNKALPAPIETKISKAKGQPREPQVYTLPPSREE 237

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QY 441 QGQNVFSCSMHREALNHYTKQSLSLSPGK 470
Db 298 QGQNVFSCSMHREALNHYTKQSLSLSPGK 327

RESULT 4
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ID GC_RABIT STANDARD; PRT; 323 AA.
AC F01870;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG GAMMA CHAIN C REGION.
OS Oryctolagus cuniculus (Rabbit).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN NCBI_TaxID=9986;
[1]
RP SEQUENCE FROM N.A.
RP MEDLINE=84030930; PubMed=63133520;
RA Bernstein K.E., Alexander C.B., Mage R.G.;
RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
RT F-1 haplotype.";
RL Immunogenetics 18:387-397(1983).
RN [2]
RP SEQUENCE OF 1-128.
RP MEDLINE=76135469; PubMed=1243651;
RA Pratt D.M., Mole L.E.;
RT "Sequence studies on the constant region of the Fd sections of rabbit
RT immunoglobulin G of different allotype.";
RL Biochem. J. 151:337-349(1975).
RN [3]
RP SEQUENCE OF 88-266 FROM N.A.
RP MEDLINE=83299917; PubMed=6193512;
RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma
RT heavy chain and identification of two genomic C gamma genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
RN [4]
RP SEQUENCE OF 132-161.
RP MEDLINE=70110015; PubMed=5461106;
RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
RT "Sequence studies of the Fd section of the heavy chain of rabbit
RT immunoglobulin G.";
RL Biochem. J. 116:249-259(1970).
RN [5]
RP SEQUENCE OF 129-131 AND 155-322.
RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
RL (In) Killander J. (eds.);
RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
RL Stockholm (1967).
CC -!- MISCELLANEOUS; REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,
CC 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
CC MARKERS AND REF.5 THE E15 MARKER.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M16426; AAA31289.1; -.
DR PIR; A02161; GHRB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IgC1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT VARIANT 104 104 T -> M (IN D11 MARKER).
FT VARIANT 185 185 T -> A (IN E15 MARKER).
FT CONFLICT 48 48 N -> E (IN REF. 2).
FT CONFLICT 71 71 V -> VPV (IN REF. 2).
FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).
FT CONFLICT 173 173 N -> D (IN REF. 5).
FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).
FT CONFLICT 201 201 N -> D (IN REF. 5).
FT CONFLICT 218 218 Q -> E (IN REF. 5).
FT CONFLICT 233 233 E -> Q (IN REF. 5).
FT CONFLICT 246 246 N -> D (IN REF. 5).
FT CONFLICT 256 256 E -> G (IN REF. 5).
FT CONFLICT 260 260 N -> D (IN REF. 5).
FT CONFLICT 266 266 N -> D (IN REF. 5).
FT CONFLICT 280 280 Y -> W (IN REF. 5).

```


OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE (DISEASE PROTEIN WIS).
 RA MEDLINE=81021548; PubMed=6774747;
 RX Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
 RT "Primary structure of human gamma 3 immunoglobulin deletion mutant:
 RT gamma 3 heavy-chain disease protein Wis.";
 RL Biochemistry 19:4304-4308(1980).
 RN [2]
 RP REVISIONS TO 12-97 OF PROTEIN WIS.
 RX MEDLINE=77118561; PubMed=402363;
 RA Michaelson T.E., Frangione B., Franklin E.C.;
 RT "Primary structure of the 'hinge' region of human IgG3. Probable
 RT quadruplication of a 15-amino acid residue basic unit.";
 RL J. Biol. Chem. 252:883-889(1977).
 RN [3]
 RP REVISIONS TO 59-289 OF PROTEIN WIS (DISEASE PROTEIN ZUC).
 RX MEDLINE=77021516; PubMed=823945;
 RA Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;
 RT "The amino acid sequence of 'heavy chain disease' protein ZUC.
 RT Structure of the C₁ fragment of immunoglobulin G3.";
 RL Biochem. Biophys. Res. Commun. 71:907-914(1976).
 RN [4]
 RP SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
 RX MEDLINE=82247835; PubMed=6808505;
 RA Alexander A., Steinmetz M., Barritault D., Frangione B.,
 RA Franklin E.C., Hood L., Ruxbaum J.N.;
 RT "Gamma heavy chain disease in man: CDNA sequence supports partial
 RT gene deletion model.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
 CC -1- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
 CC INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
 CC NORMALLY PRESENT IN THE HINGE REGION.
 CC -1- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
 CC -1- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
 CC REF.2.
 CC -1- MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION
 CC AND ALL OF THE CH1 REGION.
 CC -1- MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL
 CC OF THE CH1 REGION, AND PART OF THE HINGE COMPARED WITH NORMAL
 CC GAMMA-3 HEAVY CHAINS.
 CC -1- MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM
 CC OR ANOTHER GAMMA CHAIN SUBCLASS.
 CC -1- MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR
 CC TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE
 CC IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
 CC SEGMENT (12-28).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: J00231; AAA52805.1; ALT_SEQ.
 CC PIR: A02149; G3HWT.
 CC MIM: 147120;
 CC InterPro: IPR003006; Ig_MHC.
 CC InterPro: IPR003597; Ig_c1.
 CC InterPro: IPR003600; Ig_like.
 CC Pfam: PF00047; Ig; 2.
 CC SMART: SM00407; IgC1; 1.
 CC SMART: SM00410; IgC1; 1.
 CC PROSITE: PS00290; IG_MHC; 1.
 CC Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
 KW DOMAIN 12 73 HINGE.
 FT DOMAIN 74 183 CH2.
 FT DOMAIN 184 289 CH3.

FT	REPEAT	29	43
FT REPEAT	44	58	
FT REPEAT	59	73	
FT MOD_RES	1	1	
FT CARBOHYD	6	6	
FT DISULFID	7	7	
FT DISULFID	24	24	
FT DISULFID	27	27	
FT DISULFID	33	33	
FT DISULFID	39	39	
FT DISULFID	42	42	
FT DISULFID	48	48	
FT DISULFID	54	54	
FT DISULFID	57	57	
FT DISULFID	63	63	
FT DISULFID	69	69	
FT DISULFID	72	72	
FT CARBOHYD	140	140	
FT MOD_RES	290	290	
FT VARIANT	126	127	
FT VARIANT	134	134	
FT VARIANT	139	139	
FT VARIANT	182	182	
FT VARIANT	227	227	
FT VARIANT	227	227	
FT VARIANT	279	279	
FT SEQUENCE	290 AA; 32331 MW; E69CB95705B2F46 CRC64;		

Query Match 46.2%; Score 1162; DB 1; Length 290;
 Best Local Similarity 91.4%; Pred. No. 6.4e-73;
 Matches 212; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY	239	EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF	298
Db	59	EPKSCDTPPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF	118
QY	299	NWYVDGVEVHNAKTKPREEQNTSYRYVSVLTVLDQWLNQKEYCKVSNKALPAPIEKT	358
Db	119	KWYVDGVQVHNATKPREQNFSTFRVSVLTVLDQWLNQKEYCKVSNKALPAPIEKT	178
QY	359	ISKAKGPREPQVYTLPPSREEMTKNQVSLTCLVKGYGSPIDIAVWESNGOPENNYKTPP	418
Db	179	ISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGYGSPIDIAVWESNGOPENNYKTPP	238
QY	419	PVLDSGSRFLYSLKLTVDKSRWQGNVFCGSMHEALHNYHTOKLSLSPGK	470
Db	239	PMLDSGSRFLYSLKLTVDKSRWQGNVFCGSMHEALHNYHTOKLSLSPGK	290

RESULT	7
GCL_RAT	STANDARD; PRT; 326 AA.
ID	AC P20759;
DT	01-FEB-1991 (Rel. 17, Created)
DT	01-FEB-1991 (Rel. 17, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	IG GAMMA-1 CHAIN C REGION.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX	NCBI_TaxID=10116;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=89232738; PubMed=3149946;
RA	Brueggemann M.;

RT *Evolution of the rat immunoglobulin gamma heavy-chain gene family.*;
 RL Gene 74:473-482(1988).

DR PIR: PS0017; PS0017.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_C1.
 DR Pfam: PF00047; Ig; 3.
 DR SMART: SM00407; Ig; 2.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
 FT NON_TER 1 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 112 HINGE.
 FT DOMAIN 113 219 CH2.
 FT DOMAIN 220 326 CH3.
 FT DISULFID 27 82
 FT DISULFID 102 102
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 140 200
 FT DISULFID 246 304
 FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;

Query Match 45.98; Score 1155; DB 1; Length 326;
 Best Local Similarity 63.4%; Pred. No. 2.3e-72;
 Matches 211; Conservative 52; Mismatches 60; Indels 10; Gaps 4;

QY 141 ASTRGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSVHTFPAVLQSS 200
 DB 1 AETAPSVYPLAPGTALKSNMWLGCLVKGYFPEPTVYVWNSGALSGVHTFPAVLQ-S 59
 QY 201 GLYSLSVTVTPSSSLGRTYICNVNHPKNTKVDKRPKSCDKTHPCPCPAPELIGG 260
 DB 60 GLYTLTSSVTPSSWPSQVTCNVAHPASSTKVDDKIVPRNCG--GDCKPC----ICTG 113
 QY 261 ---PSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKNWYVDGVEVINAKTKPRE 317
 DB 114 SEVSVVTFPPPKPKDVLITLTTPKVTCTVVDVSHEDPEVKNWYVDGVEVINAKTKPRE 173
 QY 318 QYNSTYRVSVLTVLHODWLNKGEYCKVSNKALPAPAEIKTISKAKGPQRPQVYTLPPS 377
 DB 174 QFNSTFRVSSELPILHODWLNKGRFRCKVTSAAPSPSEIKTISKPEGTQVPHVTMGPT 233
 QY 378 REEMTKNOVSLTCLVKGYFSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 437
 DB 234 KEEMTQNEVSTCMVKGYPYDIIVWQMNGQPQENYKNTPTPTMDTSGSYFLYSKLVYK 293
 QY 438 SRWQGNVFCSCVMHEALHNHYTKQSLSPGK 470
 DB 294 EKWQGNVFTCTSVLHGLHNHHTKSLSPGK 326

RESULT 8
 GC3_MOUSE STANDARD; PRT; 329 AA.
 AC GC3_MOUSE
 AC P22436;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE IG GAMMA-3 CHAIN C REGION, SECRETED FORM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85027161; PubMed=6092053;
 RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
 RA Tucker P.W., Blattner F.R.;
 RT "Structural analysis of the murine IgG3 constant region gene".
 RL EMBO J. 3:2041-2046(1984).

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CC -----
 CC EMBL; J00451; -; NOT_ANNOTATED_CDS.
 DR PIR: B02156; G3MSC.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_C1.
 DR InterPro: IPR003600; Ig_Like.
 DR Pfam: PF00047; Ig; 3.
 DR SMART: SM00407; Ig; 2.
 DR SMART: SM00410; IG_Like; 1.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Transmembrane; Alternative splicing.
 FT NON_TER 1 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 113 HINGE.
 FT DOMAIN 114 223 CH2.
 FT DOMAIN 224 327 CH3.
 SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match 45.7%; Score 1150; DB 1; Length 329;
 Best Local Similarity 65.0%; Pred. No. 5e-72;
 Matches 215; Conservative 44; Mismatches 68; Indels 4; Gaps 3;

QY 142 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSVHTFPAVLQSSG 201
 DB 1 TTAPSVYPLVPGCDSTSGSVTLGCLVKGYFPEPTVYVWNSGALSGVHTFPAVLQ-SG 59
 QY 202 LYSLSVTVTPSSSLGRTYICNVNHPKNTKVDKRPKSCDKTHPC--PCPAPELIG 259
 DB 60 FYLSLSVTVTPSSWPSQVTCNVAHPASSTKELIKRIEPR-IPKPSPTPPGSSCPGNIIG 118
 QY 260 GPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKNWYVDGVEVINAKTKPREQY 319
 DB 119 GPSVFIFFPKPKDALMISLTTPKVTCTVVDVSHEDPEVKNWYVDGVEVINAKTKPREQY 178
 QY 320 NSTYRVSVLTVLHODWLNKGEYCKVSNKALPAPAEIKTISKAKGPQRPQVYTLPPSPS 379
 DB 179 NSTFRVSSELPILHODWLNKGRFRCKVTSAAPSPSEIKTISKPEGTQVPHVTMGPT 238
 QY 380 EMTKNQVSLTCLVKGYFSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 439
 DB 239 QMSKKKSLTCLVTNFFSEASVEMERNGELEQDYKNTPTPTMDTSGTYFLYSKLTVDTS 298
 QY 440 WQGNVFCSCVMHEALHNHYTKQSLSPGK 470
 DB 299 WQGEIFCTSVVHEALHNHHTQKLSRSPGK 329

RESULT 9
 GCL_MOUSE STANDARD; PRT; 324 AA.
 ID GCL_MOUSE
 AC P01868;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE IG GAMMA-1 CHAIN C REGION.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=80045036; PubMed=115593;
 RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,

Matches 214; Conservative 45; Mismatches 68; Indels 9; Gaps 3;

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QY 141 ASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVVTVSNWNGALTSVHTFPAVLQSS 200
Db 1 AQTTPSYVPLAPGCGDTSSTVTGLCLVKGYFPEPVVTVSNWNGALSSDVHTFPAVLQ-S 59
QY 201 GLYSLSVVTVPSSSLGTQTYICNVNHRKPSNTKVDKRVPEKS-----CDKTHTCPPCPA 254
Db 60 GLYTLTSSVT--SSTWPSQVTCVNAHPASSTKVDKRVKERRNGGIGHKPCPTCKHCPV 117
QY 255 PELLGGPSVFLFPKPKDFTLMISRTPEVTVVVDVSHEDPEVKFMYVDGVEVHNNAKTP 314
Db 118 PELLGGPSVFLFPKPKDFTLMISRTPEVTVVVDVSEBEPDQVQSFVNNVEVHTAQTP 177
QY 315 REEQYNSTRYRVVSLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 374
Db 178 REEQYNSTRYRVVSLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 237
QY 375 PPSREMTKNOVSLTCLVKGYFPEPVVTVSNWNGALTSVHTFPAVLQSS 434
Db 238 GPTEQLTEQVSLTCLVSGFLPNDIGVEWTSNGHIEKNYKTEPVPDSDGSGFFMISKLN 297
QY 435 VDKSRWQGNVFCSSVMHEALHNHYTQKSLSLSPGK 470
Db 298 VERSRWDSRAPEVCSVVHEGLHNHHEKSIKSRPPCK 333
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RESULT 11

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GC1M_MOUSE STANDARD; PRT; 393 AA.
AC P01869;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE IG GAMMA-1 CHAIN C REGION, MEMBRANE-BOUND FORM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
RN Cell 18:559-568(1979).
[2]
RP SEQUENCE OF 323-393 FROM N.A.
RX MEDLINE=82197626; PubMed=6804950;
RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
RT "mRNA for surface immunoglobulin gamma chains encodes a highly
conserved transmembrane sequence and a 28-residue intracellular
domain.";
RN proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
[3]
RP SEQUENCE OF 323-366 FROM N.A.
RX MEDLINE=82115295; PubMed=6799207;
RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
RA Eisenberg D., Wall R.;
RT "Gene segments encoding transmembrane carboxyl termini of
immunoglobulin gamma chains.";
RN Cell 26:19-27(1981).
[4]
RP SEQUENCE OF 1-44 FROM N.A.
RX MEDLINE=8222190; PubMed=6283537;
RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
immunoglobulin gamma chains.";
RN proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC -1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
```

CC BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
CC IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
CC SEGMENT OF MU CHAINS.

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DR EMBL; V00793; CAA24172.1; -
DR EMBL; V00793; CAA24173.1; -
DR EMBL; V00793; CAA24174.1; -
DR PIR; B02159; GIMSM.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR003006; Igh_MHC.
DR InterPro; IPR003597; Igh_c1.
DR Pfam; PF00047; Igh; 3.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing; Transmembrane.
FT NON_TER 1
FT DOMAIN 1 97
FT DOMAIN 98 110
FT DOMAIN 111 217
FT DOMAIN 218 324
FT DISULFID 27 82
FT DISULFID 102 102
FT DISULFID 104 104
FT DISULFID 107 107
FT DISULFID 109 109
FT DISULFID 138 198
FT CARBOHYD 174 174
FT DISULFID 244 302
FT DISULFID 340 357
FT TRANSMEM 358 393
FT DOMAIN 393 438
SQ SEQUENCE 393 AA; 43386 MW; 4CC88343B7AICE27 CRC64;
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Query Match 45.3%; Score 1140; DB 1; Length 393;

Best Local Similarity 62.2%; Pred. No. 3.1e-71;

Matches 206; Conservative 55; Mismatches 60; Indels 10; Gaps 4;

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QY 141 ASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVVTVSNWNGALTSVHTFPAVLQSS 200
Db 1 AKTTPSYVPLAPGCGDTSSTVTGLCLVKGYFPEPVVTVSNWNGALSSDVHTFPAVLQSD 60
QY 201 GLYSLSVVTVPSSSLGTQTYICNVNHRKPSNTKVDKRVPEKSCKDHTHTCPP--CPAPELL 258
Db 61 -LYTLSSSVTVPSRPSRSETVTCVNAHPASSTKVDKRVPRDCG----CKPCICTVPEV- 114
QY 259 GQPSVFLPFPKPKDFTLMISRTPEVTVVVDVSHEDPEVKFMYVDGVEVHNNAKTPREQ 318
Db 115 --SSVFIFFPKPKDFTLTITPKVTCVVDVSDKDDPEVQFSWFVDDVEVHTAQTPREQ 172
QY 319 YNSTYRVVSLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
Db 173 FNSTRSVSELPIMHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 232
QY 379 EEMTKNOVSLTCLVKGYFPEPVVTVSNWNGALTSVHTFPAVLQSS 438
Db 233 EQMAKDKVSLTCMITDFFPEDITVEWQNGQPAENYKNTQPTMNTNGSYFVYSKLVNYS 292
QY 439 RMOQGNVFCSSVMHEALHNHYTQKSLSLSPG 469
Db 293 NWEAGNTFTCSVLHEGLHNHHEKSIKSRPPCK 323
```

RESULT 12

GC3M_MOUSE

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=82037861; PubMed=6170065;
RA Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
RT "Multiple differences between the nucleic acid sequences of the
IgG2aa and IgG2ab alleles of the mouse.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
RN [2]
RP SEQUENCE.
RX MEDLINE=82037777; PubMed=6794027;
RA Dognin M.J., Lauwereys M., Strosberg A.D.;
RT "Multiple amino acid substitutions between murine gamma 2a heavy
chain fc regions of Ig1a and Ig1b allotypic forms.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC -1- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
CC FROM BALB/C MICE, AT 15% OF THE POSITIONS.
CC -----
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CC -----
DR EMBL; J00479; -; NOT_ANNOTATED_CDS.
DR PIR; A02153; G2MSAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IgC1; 2.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
SQ SEQUENCE 335 AA; 36596 MW; FA3382792CBB13C6 CRC64;

Query Match 44.8%; Score 1126.5; DB 1; Length 335;
Best Local Similarity 61.6%; Pred. No. 2.1e-70;
Matches 207; Conservative 52; Mismatches 70; Indels 7; Gaps 2;

QY 141 ASTKGPSVFPLAPSSKSTSGGTAAALGLVDPYPPVTVSWNSGALTSGVHTFPVAVLQSS 200
Db 1 AKTTAPSVYPLVPVCGGTGSSVTGLCLVKGYRPEPTLTWNSGSLSSGVHTFPALLQ-S 59

QY 201 GLYSLSSVTVPSSSLGTQYIYICNVNHNKPSNTKVDRKVEPK-----SCDKTHTCPPCPA 254
Db 60 GLYTLSSSVTVTSNTWPSQTITCNVAHPASSTKVDRKIEPRVPTQNPCPPHORVPVPCAA 119

QY 255 PELLGGPSVFPLPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKP 314
Db 120 PDLGGPSVFIFPPKIKDVLMLISLSPVTCVVVDSEDDPDVQLISWVFNNEVHTAQTQT 179

QY 315 REEYNSYTRVSWVLTVLHODWLNKEYCKVSNKALPAPIEKTIISKAKGPREPQVYTL 374
Db 180 HREDYNSLTRVVSALPIQHODWMSGKEFKCKVNNRALPSPIEKTIISKPRGVRAPQVYL 239

QY 375 PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPTPVLDSGSEFLYSKLT 434
Db 240 PPAPEAMTKKEFSLTCLMITGFLPAETAVDWTNSGRTEQNYKNTATVLDSGSEYFMYSKLR 299

QY 435 VDKSRWOGNVFSCSVNMEALHNHYTOKSLSLSPGK 470
Db 300 VQKSTWERSGLFACSVVHEVLHNLHTTKTISRSLGK 335

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 17, 2002, 16:40:41 ; Search time 40.91 Seconds
(without alignments)
1680.469 Million cell updates/sec

Title: US-09-499-662-117
Perfect score: 2517
Sequence: 1 MGWSCILFLVATATGVHSQ.....MHEALHHYTKSLSPGK 470

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL.17:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mbc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match %	Length	DB	ID	Description
1	1636.5	65.0	473	11	Q9D8L4	Q9d8l4 mus musculus
2	1625.5	64.6	463	11	Q99LC4	Q99lc4 mus musculus
3	1585.5	63.0	473	11	Q99L25	Q99l25 mus musculus
4	1559	61.9	468	11	Q99L31	Q99l31 mus musculus
5	1433.5	57.0	437	11	Q9RIA4	Q9ria4 mus musculus
6	859	34.1	500	4	Q9BRV0	Q9brv0 homo sapien
7	759.5	30.2	597	4	Q9BU10	Q9bu10 homo sapien
8	755.5	30.0	597	4	Q9BQ88	Q9bq88 homo sapien
9	755	30.0	484	11	Q99LA6	Q99la6 mus musculus
10	721.5	28.7	487	11	Q99KA4	Q99ka4 mus musculus
11	649	25.8	479	11	Q99M22	Q99m22 mus musculus
12	602	23.9	426	11	Q9DCD9	Q9dcd9 mus musculus
13	577.5	22.9	416	4	Q9NPP6	Q9npp6 homo sapien
14	522	20.7	150	4	Q9Y298	Q9y298 homo sapien
15	505	20.1	157	4	Q95978	Q95978 homo sapien
16	480.5	19.1	384	4	Q9UP60	Q9up60 homo sapien
17	466	18.5	119	4	Q9UL94	Q9ul94 homo sapien
18	465.5	18.5	124	4	Q9UL92	Q9ul92 homo sapien
19	455	18.1	117	11	Q9QXF0	Q9qxfo mus musculus

20	454	18.0	119	5	Q9QY22	Q9qyz2 schistosoma
21	452	18.0	125	4	Q9UL95	Q9ul95 homo sapien
22	445.5	17.7	116	4	Q9UL89	Q9ul89 homo sapien
23	441.5	17.5	118	11	Q9Z1C4	Q9z1c4 mus musculus
24	439	17.4	117	11	Q9QXE9	Q9qxe9 mus musculus
25	437.5	17.4	114	11	Q9JL81	Q9jl81 mus musculus
26	436.5	17.3	147	4	Q9Y509	Q9y509 homo sapien
27	433.5	17.2	110	11	Q9JL77	Q9jl77 mus musculus
28	417	16.6	111	11	Q9D988	Q9d988 mus musculus
29	415.5	16.5	109	11	Q9JL75	Q9jl75 mus musculus
30	400	15.9	117	11	Q9Z1C6	Q9z1c6 mus musculus
31	399	15.9	375	4	Q9BS21	Q9bsz1 homo sapien
32	393	15.6	684	13	Q90544	Q90544 ginglymosto
33	385.5	15.3	110	11	Q9JL83	Q9jl83 mus musculus
34	371.5	14.8	298	11	Q9QYF0	Q9qyf0 mus musculus
35	357	14.2	120	4	Q9BUA1	Q9bua1 homo sapien
36	356	14.1	109	11	Q9JL85	Q9jl85 mus musculus
37	333	13.2	113	4	Q9UL90	Q9ul90 homo sapien
38	324	12.9	121	4	Q9UL71	Q9ul71 homo sapien
39	323.5	12.9	118	4	Q9UL91	Q9ul91 homo sapien
40	323	12.8	131	4	Q9UL88	Q9ul88 homo sapien
41	320.5	12.7	112	4	Q9HCC1	Q9hcc1 homo sapien
42	315.5	12.5	122	4	Q9UL84	Q9ul84 homo sapien
43	314	12.5	116	4	Q9UL93	Q9ul93 homo sapien
44	306.5	12.2	118	4	Q9UL72	Q9ul72 homo sapien
45	302.5	12.0	150	4	Q95973	Q95973 homo sapien

ALIGNMENTS

RESULT	ID	PRELIMINARY;	PRT;	473 AA.
Q9D8L4	Q9D8L4			
AC	Q9D8L4;			
DT	01-JUN-2001 (Tremblrel. 17, Created)			
DT	01-JUN-2001 (Tremblrel. 17, Last sequence update)			
DT	01-JUN-2001 (Tremblrel. 17, Last annotation update)			
DE	1810060009RIK PROTEIN.			
GN	1810060009RIK.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=PANCREAS;			
RX	MEDLINE=21085660; PubMed=11217851;			
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,			
RA	Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,			
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,			
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,			
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,			
RA	Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,			
RA	Schriml L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,			
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,			
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,			
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,			
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,			
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,			
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,			
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,			
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,			
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,			
RA	Havashizaki Y.;			
RT	"Functional annotation of a full-length mouse cDNA collection.";			
RL	Nature 409:685-690(2001).			
CC	-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX			
CC	DOMAIN.			
DR	EMBL; AK007918; BAB25349.1; "			
DR	MGI; 1924014; 1810060009RIK.			
DR	InterPro; IPR003599; Ig.			

DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00409; Ig_2.
DR SMART; SM00407; Igcl; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; Ig_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 65.0%; Score 1636.5; DB 11; Length 473;
Best Local Similarity 63.7%; Pred. No. 3.5e-124;
Matches 303; Conservative 70; Mismatches 94; Indels 9; Gaps 4;

QY 1 MGWSCIILFLVATATGVHVSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKQAP 60
Db 1 MEWSWFLFLSVTAGVHCQVQLQSGAEELVPGASVKISCKASGYTFTSYMMQWVKQAP 60
QY 61 GQGLEWNGEIDPDSYTYNOKFKGKATLTVDSTSTAYMELSLRSRSEDYAVYCARNRD 120
Db 61 GQGLEWIKIGPGSGSYTYNEKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCARS-G 119
QY 121 YSNWYFDVWGEGLTVTVSSASTKGPVFPPLAPSKSTSGGTAALGCLVKDYFPEPVTVS 180
Db 121 YSDYDWFAYWCGQGLTVTVSSAAKTTAPSVYPLAPVCGGTGSSVTLGCLVKGYFPEPVTLT 178
QY 181 WNSGALTSQVHTFPVAVLQSGSLYSLSVTVTPSSSLGTQTYICNVNKKPSTKVDKRVKPE 240
Db 179 WNSGSLSGVHTFPVAVLQSGSLYSLSVTVTPSSSLGTQTYICNVNKKPSTKVDKRVKPE 237
QY 241 K-----SCDKTHPCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP 294
Db 238 RVPITQNPCLPKPCPCPAAPDLGGPSVFIFPPKIKDVLMSLSPVTCVVDVSEDDP 297
QY 295 EVKFNWYDGEVHNATKPREQYNSTYRVVSVLTVLDHQLNGKEYKCKVSKNKAALPAP 354
Db 298 DVQISWFNWYVHTAQTHREDYNSLTRVVSALPQHQQDMSGKEFKCKVNNRALPSP 357
QY 355 IEKTIKAKGQPREPVYTPPPSREEMTKNOVSLTCLVKGFPYSDIAVEWESNGQPENNY 414
Db 358 IEKTIKPRGVPVAPQVYVLPAPAEETKKEFSLTCLMTITGLPAEIAVDVTSNGRTQNY 417
QY 415 KTTPLVLDGSGFFLYSKLTVDKSRWQGNVFCVSMHEALHNHYTKSLSPGK 470
Db 418 KNTATVLDGSGYPMYSLKRVQKSTWERSGLFACSVVHGLHNLHTTKTISRSLGK 473

RESULT 2

QY99LC4 ID Q99LC4 PRELIMINARY; PRT; 463 AA.
AC Q99LC4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1; -.
SQ SEQUENCE 463 AA; 51007 MW; BAA674C6BBBC30783 CRC64;

Query Match 64.6%; Score 1625.5; DB 11; Length 463;
Best Local Similarity 63.6%; Pred. No. 2.7e-123;
Matches 300; Conservative 72; Mismatches 89; Indels 11; Gaps 5;

QY 1 MGWSCIILFLVATATGVHVSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKQAP 60
Db 1 MEWIIWELFILSFTAGVHVSQVQLQSGAEELVPGASVKISCKASGYTFTSYMMQWVKQAP 60
QY 61 GQGLEWNGEIDPDSYTYNOKFKGKATLTVDSTSTAYMELSLRSRSEDYAVYCARNRD 120
Db 61 GQGLEWNGEITYPGSGNTYTYSEKFKGKATLTADKSSSTAYMHLSLTSDSAVYFCARSY 120
QY 121 YSNWYFDVWGEGLTVTVSSASTKGPVFPPLAPSKSTSGGTAALGCLVKDYFPEPVTVS 180
Db 121 YSYD-LFAYWCGQGLTVTVSSAAKTTAPSVYPLAPGSAAGTNSMTLGLCLVKGYFPEPVTVT 179
QY 181 WNSGALTSQVHTFPVAVLQSGSLYSLSVTVTPSSSLGTQTYICNVNKKPSTKVDKRVKPE 240
Db 180 WNSGSLSGVHTFPVAVLQSD-LYTLSSSVTVPSSTWSPSETVTCNVHAPASSTKVDKRVK 238
QY 241 KSCDKTHPCPP--CPAPELGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 298
Db 239 RDCG---CKPICICTVPEV---SSVFIFPPKPKDVLITLTPKVTCTVVDVSKDDPEVQF 291
QY 299 NWYDGEVHNATKPREQYNSTYRVVSVLTVLDHQLNGKEYKCKVSKNKAALPAPTEKT 358
Db 292 SWFVDDVEVHTAQTPREQFNSTFRVSELPIMHQDLNGKEFKCRVNSAATFPAPIEKT 351
QY 359 ISKAGQPREPVYTPPPSREEMTKNOVSLTCLVKGFPYSDIAVEWESNGQPENNYKTP 418
Db 352 ISKTKGRPKAPQVYTIPTPKQMAKDKVSLTCLMTITDFPEDITVWQWNGQPAENYKNTQ 411
QY 419 PVLDSGSGFFLYSKLTVDKSRWQGNVFCVSMHEALHNHYTKSLSPGK 470
Db 412 PIMTDGSGYFIYSLKLVQKSNWEAGNTFTCSVLHEGLHNLHHTKSLSHSPGK 463

RESULT 3

QY99L25 ID Q99L25 PRELIMINARY; PRT; 473 AA.
AC Q99L25;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003888; AAH03888.1; -.
SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match 63.0%; Score 1585.5; DB 11; Length 473;
Best Local Similarity 63.4%; Pred. No. 4.7e-120;
Matches 301; Conservative 61; Mismatches 106; Indels 7; Gaps 5;

QY 1 MGWSCIILFLVATATGVHVSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKQAP 60
Db 1 MEWSWFLFLSVTVTVHVSQVQLQSGAEELVPGASVKISCKASGYTFTDTHTHHWKQRP 60
QY 61 GQGLEWNGEIDPDSYTYNOKFKGKATLTVDSTSTAYMELSLRSRSEDYAVYCARNRD 120
Db 61 EQGLEWIGYIVPRDGSYTYNEKFKGKATLTADKSSSTAYMQLNSLTSDSAVCFCSRGS 120
QY 121 --YSNN-WYFDVWGEGLTVTVSSASTKGPVFPPLAPSKSTSGGTAALGCLVKDYFPEPV 177
Db 121 IYIGYGLYFDYWGQGTITVSSAKTTAPSVYPLAPVCGDGTGSSVTLGCLVKGYFPEPV 180
QY 178 TVSNWNSGALTSQVHTFPVAVLQSGSLYSLSVTVTPSSSLGTQTYICNVNKKPSTKVDKR 237
Db 181 TLWNNSGSLSGVHTFPVAVLQSD-LYTLSSSVTVTPSSVTSQSITCNVAHPASSTKVDKK 239


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Qy 238 VEPKSCDKTHTCPP--CPAPELGGPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPE 295
Db 240 IEPRG-PTIKPCPPCKPAPNLLGGPSVFIIPPKKIKDGLMISLSPMWTCVVVDVSHEDPD 298
Qy 296 VKFNWYDGVVHNNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 355
Db 299 VOISWVNNVEVLTAOTQTHREDYNSTRVVSALPIQHODWMSGKEFKCKVNNKALPAPI 358
Qy 356 EKTISKAKGQPREPOVYLLPPSRREMTKNQVSLCLVKLGKFPDIAVWESNGQPENNYK 415
Db 359 ERTISKPGSVRAQVYVLPPEEMTKKQVLTCLMVDFPEDIYVETWNGKTELNYK 418
Qy 416 TTPPVLDSDGSFELYKLTVDKSRWQOGNFCVSCVMHEALHNHYTKSLSLSPGK 470
Db 419 NTEPVLDSDGSFYMSKURVEKKNWERNYSYSCVVHGEGLHNHHTTKSFSRTPGK 473

RESULT 4
ID Q99L31 PRELIMINARY; PRT; 468 AA.
AC Q99L31;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AA040387.1; -.
SQ SEQUENCE 468 AA; 51661 MW; 96352323B3332ADB CRC64;
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```
Query Match 61.98; Score 1559; DB 11; Length 468;
Best Local Similarity 62.79; Pred. No. 6.4e-118;
Matches 296; Conservative 62; Mismatches 108; Indels 6; Gaps 4;

Qy 1 MGWSCIILFVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKAP 60
Db 1 MKCSWVIFFLNAVIGVNSEVQLQSGAEVLRPGASVKLSCTASGFKLSDLMHWVKORP 60
Qy 61 GQGLEWMEIDPSDSTYNQKFKGKATLVDTSTSTAYMELSLRSDEDTAVYYCARNRD 120
Db 61 EQGLEWIGWIDPGETKYAPKFDQKATITADTSSNTAYLQLSLTSEDTAIYYCARNLL 120
Qy 121 YSNWYFDVWEGEGLTVTVSSASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPVTVS 180
Db 121 YGG--YYDYWGQGTITVSSAKTTPSYVPLAPVCGDPTGSSVTLGCLVKGYFPEPVTLT 178
Qy 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTOTICNVNHPKSTKVDKRVPE 240
Db 179 WNSGSLSCSVHTFPAVLQSD--LYTLSSSVTVTPSTWPSQSTCNVAHPASSTKVDKKTLEP 237
Qy 241 KSCDKHTHCP--CPAPELGGPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKF 298
Db 238 RG-PTIKPCPPCKPAPNLLGGPSVFIIPPKKIKDGLMISLSPMWTCVVVDVSHEDPDVQI 296
Qy 299 NNYVDGVVHNNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIBKT 358
Db 297 SWFNWVNNVEVLTAOTQTHREDYNSTRVVSALPIQHODWMSGKEFKCKVNNKALPAPIERT 356
Qy 359 ISKAGQPREPOVYLLPPSRREMTKNQVSLCLVKGFYPSDIAVWESNGQPENNYKTPP 418
Db 357 ISKPGSVRAQVYVLPPEEMTKKQVLTCLMVDFPEDIYVETWNGKTELNYKTE 416
Qy 419 PVLDSDGSFELYKLTVDKSRWQOGNFCVSCVMHEALHNHYTKSLSLSPGK 470
Db 417 PVLDSDGSFYMSKURVEKKNWERNYSYSCVVHGEGLHNHHTTKSFSRTPGK 468
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```
RESULT 5
Q9RIA4
ID Q9RIA4 PRELIMINARY; PRT; 437 AA.
AC Q9RIA4;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE GAMMAL HEAVY CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G.; Yu X.; Ekramoddoullah A.K.M.; Misra S.;
RL "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFV).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF152372; AAD40243.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;
```

```
Query Match 57.08; Score 1433.5; DB 11; Length 437;
Best Local Similarity 59.18; Pred. No. 8.1e-108;
Matches 267; Conservative 72; Mismatches 96; Indels 17; Gaps 7;

Qy 21 VOLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKAPGQGLEWMGEIDPSDSTYN 80
Db 1 VOLQESGGLVKPGGSLKLSCAASGFTSSYAMSVRQTPEKRLWVASFS--SGGIYYT 59
Qy 81 QKFKGKATLVDTSTSTAYMELSLRSDEDTAVYYCARNRDYSNNWYFDVWEGEGLTVTVSS 140
Db 60 DSVKGRFTIYKDKRNILSLQMSLSRSEDYAMVCARG-DYS----AYWGPGLTVTVSA 113
Qy 141 ASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPVTVSNWNGALTSGVHTFPAVLQSS 200
Db 114 AKTTPSYVPLAPGSAQTNSMVTILGCLVKGYFPEPVTVSNWNGSLSGVHTFPAVLQSD 173
Qy 201 GLYSLSSVTVTPSSSLGTOTICNVNHPKSTKVDKRVPEKSCDKHTHCP--CPAPELL 258
Db 174 -LYTLSSSVTVTPSTWPSQSTCNVAHPASSTKVDKRVPRDCG---CKPICITVPEV- 227
Qy 259 GGPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVVHNNAKTPREEQ 318
Db 228 --SSVFIIPPCKDGLTITLTPKVTVCVVVDISKDDPEVQFSWFVDVDEVHTAQTQPREQ 285
Qy 319 YNSIYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYLLPPSR 378
Db 286 FNSTFRSSELPIMHQDWLNGKEFKCRVNSAFAFPAPIEKTISKTKGRKPAQVYITIPPK 345
Qy 379 EEMTKNOYSLCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFELYKLTVDK 438
Db 346 EQMAKDKVSLCTMTDFPEDIYVETWNGQPAENYKNTQPIMDTDGSGTFVTSKLVNOKS 405
Qy 439 RWQOGNFCVSCVMHEALHNHYTKSLSLSPGK 470
Db 406 NWEAGNTFTCSVLHGEGLHNHHTTKSLSPGK 437
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RESULT 6
Q9BRV0 PRELIMINARY; PRT; 500 AA.
AC Q9BRV0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:14588).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005951; AAH05951.1; -.
SQ SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;

Query Match 34.1%; Score 859; DB 4; Length 500;
Best Local Similarity 41.1%; Pred. No. 2.6e-61;
Matches 206; Conservative 68; Mismatches 177; Indels 50; Gaps 18;

QY 1 MGWSCIILFVATATGVSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKQAP 60
Db 1 MDWTWISILFLVAATGAQSQVHLVQSGAEVMSPCASVRVSKTGYAFHTYSIIWVQAP 60
QY 61 GQGLWGEIDPDSYTNYNQKFKGKATLVDTSTAYMELSLRSDEDTAVYYCARNR- 119
Db 61 GQGLWGWISPSDNTFRFAKFGQVTLTDTSTSYMELSLRSDDTAVYYCARYC 120
QY 120 DYS---NNWYF---DVMGEGTLTVSSASTKGPSVFPPLAPSSKSTSGTAALGCLVKDYF 173
Db 121 SYSSCONDYIIYMDVWGKGTITVSSASPTSPKVPFLSLS-TQPGNVVIACLVGQFF 179
QY 174 P-EPVTVSWNSGALTSVGHFPAVLQSSG-LYSLSSVTVTPSSS-LGTQTYICNVNHNKPS 230
Db 180 PQEPLSVTWSSESGGVATRNFPSPQDASGDLYTTSQTLTPATQCLAGKSVTCHKVY-T 238
QY 231 NTKVDKKEVPKSCDKTHTCPAPPELLGGPSVFLFPPKPK-----DTLM 275
Db 239 NPSQDVTV-----PCVPSPPTPTSPST-PPTPSPSCCHPRLSLHRLPAEDLL 285
QY 276 ISRTPEVTCTVVDVSHEDPEVKFNWYDGVGVHNAKTKPREQYNSTYRVVSLTVLHQD 335
Db 286 LGSEANLTCTLTGL-RDASGVTFWTWTPSSGK--SAVQGPDPDRDLCGCYSVSSVLSCGAEP 342
QY 336 WLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ-VSLTCLVKG 394
Db 343 WNHGKTFCTAAVPESKTPLTATLSKS-GNTFRPEVHLLPPPSSEALNELVLTCLARG 401
QY 395 FYPSDIAVESNQ--PENNYKTPPVLD-SDG--SFFLYSKLTVDKSRQOQNVFSCS 449
Db 402 FSPKDVLRVQLQSGQELPREKYLTVASRQEPSSQGTTFVAVTSLRVAADWKKGDFTSCM 461
QY 450 VMHEALHNHYTQKSLSLSPCK 470
Db 462 VGHALPLAFTQETIDRLACK 482

RESULT 7
Q9BU10 PRELIMINARY; PRT; 597 AA.
AC Q9BU10;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:1652).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

RESULT 8
Q9BOB8 PRELIMINARY; PRT; 597 AA.
AC Q9BOB8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:1905) (PROTEIN FOR MGC:1228).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=RHABDOMYOSARCOMA;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LYMPHOMA;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002963; AAH02963.1; -.
SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;
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Query Match 30.2%; Score 759.5; DB 4; Length 597;
Best Local Similarity 31.4%; Pred. No. 3.6e-53;
Matches 181; Conservative 91; Mismatches 187; Indels 117; Gaps 17;

QY 8 LFLVATATGVSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKQAPGQGLEWM 67
Db 8 LLLVAAPRWVLSQVQLQWAGLGLKSETLSLTCTGVGSGFYGSIWIRPPGKGLWMI 67
QY 68 GEIDPDSYTNYNQKFKGKATLVDTSTAYMELSLRSDEDTAVYYCAR-----NRDYS 122
Db 68 GEINHSGS-TNYPNLSKSRVTISVDTSKQLSLKSLSSVNAADTAVYYCARVITRASPTD 126
QY 123 NNWYFDVWEGTLTVSSASTKGPSVFPPLAPSSKSTSG-GTAALGCLVKDYFPFPTVSW 181
Db 127 GRYGMDVWGQGTITVTVSSGASAPFLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSW 186
QY 182 --NSGALTSGVHTTTPAVLQSGSLYSLSVTVTPSSSL--GTQTY-ICNVNHNKPSN----- 231
Db 187 KYKNNSDISSTRGPSVLR-GGKYAATSQLLPKSDVWQGTDEHVCKVQHPNGNKEKNV 245
QY 232 -----TKVDRKVEPKS-----CDKTHTCP----- 250
Db 246 PLPIVIAELPPKVSFVFPDRDGFNPKRKSLLICQATGFSRQIQVSWLRECKQVSGVTT 305
QY 251 -PCPAPELLGGPS----- 262
Db 306 DQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMTFCRVDHRLGTLTFOQNASSMCPVDQDTA 365
QY 263 --VFLFPKPKDGLMISRTPEVTCTVVDVSHEDPEVKFNWYDGVGVHNAKTKPREQYN 320
Db 366 IRVFAIPPS-FASIFLTKSKLCLVTLDTLYD-SVTISWTRQNGEAVKHTNISEHPN 423
QY 321 STYRVSVLVLVHODWLNKEYCKVSNKALPAPIEKTISKAKGQ-REPOVYTLPPSRE 379
Db 424 ATFSAVGEASTCEDDWNSEGERFTCTVHTDLPSPKQTIISRPKGVALLHRPDVYLLPPARE 483
QY 380 EMT-KNVSLTCLVKGYPSPDIADVWESNQGP--ENNYKTPPVLD--SDGSFFLYSKLT 434
Db 484 QLNLRSATITCLVTGFSPADVFQNMQRGQPLSPERYTTSAPMPEQAPGRYFAHSILT 543
QY 435 VDKSRWQGNVFSQSVMEALHNHYTQKSLSLSPCK 470
Db 544 VSEEWNTGTYTCVVAHEALPNRVTERTVDKSTGK 579
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Db 61 EKRLWATISDGGSYTYPPONVKGRETFISRDNAKNLNLYLQMSHLKSDTAMTYCARDMG 120
Qy 119 -RDYSNNMYFDWEGTLVTVSSASTGSPVFLAPSSKSTSGGTAALGCLVKDYFPE-P 176
Db 121 GSPYGGYRFYWGQGTITVSSSESARNPTIYPLT-LPRALSSDPVIGCLIHDFPFGST 179
Qy 177 VTSWNSSGALTSVHTTFFAVLQSSGLXSLSSVAVTPVSSSLGT-QTYICNVNHRKPSNTKVD 235
Db 180 MNVTWGRSGKDITTVNPPALASGGYTMSSQLTLPVCECPGESVKCSVQH---DSNAV 236
Qy 236 KRVEPKCDKTHTCPPCAPPELLGSGPSVFLFPKPKDTLMISRTPEVTCVVYVSHEDPE 295
Db 237 QELDVKCSGPPPCPPC-PSC--HPSLSQRPALD-LLGSDASLTCTLGLNRNPEGA 292
Qy 296 VKFNMYDGVNHNKTPREQYNST---YRVVSVLTVLHODWLNGKEYCKVSKYNKALP 352
Db 293 V-FTW-----EPSTGKDAVQKAVQNSCGCYSSVLPGCAERNWSGASFCKTTHPESD 346
Qy 353 APIEKTISKAGQPREQVYVLPSPREEMTKNQ-VSLTCLVKGFYPSDIAVWESNGQ-- 409
Db 347 T-LRGTIAKIVNTFPQVHLLPSPSEELALNELVSLTCLVRAFPKPEVLVRLHGNEL 405
Qy 410 -PENNYKTPVLDSDG--SFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSL 466
Db 406 SPESYLVEPLKEPEGATTYLVTSVLRSAETWKQGDQYSCVMGHEALPMNFTQKTIDR 465
Qy 467 SPGK 470
Db 466 LSGK 469

RESULT 11
Q99M22 ID Q99M22 PRELIMINARY; PRT; 479 AA.
AC Q99M22;
DT 01-JUN-2001 (TREMUREl. 17, Created)
DT 01-JUN-2001 (TREMUREl. 17, Last sequence update)
DT 01-JUN-2001 (TREMUREl. 17, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:6342).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staib F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AK002875; BAB22422.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 3.
DR SMART; SM00410; IG; 1.
DR SMART; SM00410; IG; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 426 AA; 45819 MW; 56E1275BA48F6FB1 CRC64;

Query Match 25.88; Score 649; DB 11; Length 479;
Best Local Similarity 33.88; Pred. No. 2.3e-44;
Matches 161; Conservative 89; Mismatches 194; Indels 32; Gaps 18;

Qy 7 ILFLVATATGVSQVLQVQSGAEVKKPGASVKVSCKASGYFTTS-YVMQWVKAPGQGLE 65
Db 6 LLYLLTALPGILSDVQLQESGPGLVKPSQSLSLTCTVGYTSITSGYWNWIRQPPGNKLE 65
Qy 66 WMGIDPSDSTYNTNQKFKATLTVDTSSTAYMELSSLRSEDYAVYGCARNRDYNNW 125
Db 66 WMGYIN-YDGSNNYNPSLKNRISITRDTSKNQKFLKLSVTTEDATYYCA-SRGYS--- 120
Qy 126 YFDVWGEGLTVTVSSATGKPSVFLAPSSKSTSGGTAALGCLVKDYFPE-PYTVSNNSG 184
Db 121 WFPNWGGTLTVSAESARNPTIYPLT-LPPALSSDPVIGCLIHDFPFGTMNVTWGS 179
Qy 185 ALTSGVHTFFAVLQSSGLYSLSSVTVTPVSSSLGT-QTYICNVNHRKPSNTKVRPEKSC 243
Db 180 GKDITTVNFPFALASGGRYTMSSQLTLPVCECPGESVKCSVQH-DSNPVQELDV---NC 235

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Query Match 23.9%; Score 602; DB 11; Length 426;
Best Local Similarity 32.6%; Pred. No. 1.3e-40;
Matches 157; Conservative 75; Mismatches 165; Indels 84; Gaps 16;

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Qy 244 DKHTCTPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVYVDSHEDPEVKNWYVD 303
Db 236 SGPTPPPIITPSC--QPSLSQRPALD-LLGSDASITCTLGLNRNPEGAV-FTW--- 288
Qy 304 GVEVHNKTRPREQYNST---YRVVSVLTVLHODWLNGKEYCKVSKNKPALPIEKTIS 360
Db 289 --EPSTGKDAVQKAVQNSCGCYSSVLPGCAERNWSGASFCKTTHPE-SGTITGTIA 345
Qy 361 KAKGQPREQVYVLPSPREEMTKNQ-VSLTCLVKGFYPSDIAVWESNGQ---PENNYKT 416
Db 346 KVTYVNTFPPQVHLLPSPSEELALNELVSLTCLVRAFPKPEVLVRLHGNELSPESYL 405
Qy 417 TTPVLDSDG--SFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSLSPGK 470
Db 406 EPLKEPEGATTYLVTSVLRSAETWKQGDQYSCVMGHEALPMNFTQKTIDRLSGK 461

RESULT 12
Q9DCD9 ID Q9DCD9 PRELIMINARY; PRT; 436 AA.
AC Q9DCD9;
DT 01-JUN-2001 (TREMUREl. 17, Created)
DT 01-JUN-2001 (TREMUREl. 17, Last sequence update)
DT 01-JUN-2001 (TREMUREl. 17, Last annotation update)
DE ADULT MALE KIDNEY CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE CLONE:0610041A01, FULL INSERT SEQUENCE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staib F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AK002875; BAB22422.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 3.
DR SMART; SM00410; IG; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 426 AA; 45819 MW; 56E1275BA48F6FB1 CRC64;

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QY 1 MGWSCIILFLVATATGCVHVSQVQVQSGAEVKKPGASVKVSKCASGVTFTSYWQWVKQAP 60
 DB 1 MGFSRIFLLSVTIG----- 16
 QY 61 GCGLEMMGEIDPSDYTNYNOKFKGKATLTVDSTSTAYMELSSLRSEDATVYYCARNRD 120
 DB 17 -----NGDTSYNOKFKGKATLTVDKSSSTAYMQLSSLTSEDSAYFFCARS-D 62
 QY 121 YSNWYFDVWGBGTLTVTSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPE-PVTV 179
 DB 63 YYGPTAMDYWGOGTSTVTSSESARNTIYPLT-LPRALSSDPVITGCLIHDFPSCMTMV 121
 QY 180 SNWSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGT-QTYICNVNHNKPSNTKVKRV 238
 DB 122 TWGKSGKDTITVFPALASGGCYTMSQTLTPAVECEGESVKSQVH---DSNAVQEL 178
 QY 239 EPKSCDKTHTCCPCPAPELLGCGSVFPPKPKDLMISRTPETVTVVVDVSHEDPEVKF 298
 DB 179 DVKCSGPPPPCP-PC-HPSLSLQRPALD-LLLGSDASLCTGLNLRNPEGAV-F 233
 QY 299 NWYVDGVEVHNKTKPREQYNST---YRVSVLVTLVHODWLNKGYKCKVSNKALPAPI 355
 DB 234 TW-----EPSTGKDAVQKAVQNSCGCYSVSVLPCCAEKRNWNSGAFKCTVTHPESDT-L 287
 QY 356 EKTISKAKGQPREPOVYITLPPSRREEMTKNQ-VSLTCLVKGYFSPDAVAVESWNGO---PE 411
 DB 288 TGTIAKITVTFPPQVHLLPPSEALNELVSLTCLVAFNPKVEVLVRLHNGNELSP 347
 QY 412 NNYKTTTPVLDSDG--SFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQKSLSPG 469
 DB 348 SYLVEPLKEPEGATTVLTSLVRSALWKGQGYSCMWGHEALPMNFTQKTDRLSG 407
 QY 470 K 470
 DB 408 K 408

RESULT 13
 Q9NP6 PRELIMINARY; PRT; 416 AA.
 ID Q9NP6
 AC Q9NP6
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE IMMUNOGLOBULIN HEAVY CHAIN VARIANT (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pluvinet R., Estivill X., Escarceller M., Sumoy L.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Auftray C., Ansorge W., Ballabio A., Estivill X., Gibson K.,
 RA Leirach H., Poustka A., Lundeberg J.;
 RT "The European IMAGE Consortium for Integrated Molecular analysis of
 human gene transcripts."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN
 DR EMBL; AL389978; CAB97534.1; -.
 DR InterPro; IPR003600; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_4.
 DR SMART; SM00406; IgV; 1.
 DR SMART; SM00406; IgV; 1.
 DR SMART; SM00410; IG_Like; 3.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 FT NON_TER 1
 SQ SEQUENCE 416 AA; 44786 MW; 8C41708BB8AB4687 CRC64;

Query Match 22.9%; Score 577.5; DB 4; Length 416;
 Best Local Similarity 35.2%; Pred. No. 1.2e-38;
 Matches 149; Conservative 66; Mismatches 171; Indels 37; Gaps 17;
 QY 60 PCGGLWMEIDPSDYTNYNOKFKGKATLTVDSTSTAYMELSSLRSEDATVYYCARNR 119
 DB 1 PKGGLWVSRISSGDTVDYADSVKGRFTVSRDTAKNSLSQMSLRVEDATVYYCAR-- 58
 QY 120 DYSNNWY-FDVWGBGTLTVTSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPE-EPV 177
 DB 59 -----IYGDVWYGQGTITVSSASPTSPKVPPLSLDS-TPDGNVVVACLVQGFPPQEL 113
 QY 178 TVSNWNGALTSGVHTFPAVLQSSG-LYSLSSVTVTPSSSL-GTQTYICNVNHN--KFSNTK 233
 DB 114 SVTWSGQNVTFARNPPSQDASGLDLYTSSQLTLPATQCPDGKSVTKVHKYTNPSQ-- 171
 QY 234 VDKRVEPKSCDTHRCPCPAPELLGCGSVFPPKPKDLMISRTPETVTVVVDVSHED 293
 DB 172 -----DVTVPVPPPPCC-HPRLSLHRALED-LLLGSEANLTCTLTGL-RDA 218
 QY 294 PEVKFNWYVDGVEVHNKTKPREQYNSTYRVSVLVTLVHODWLNKGYKCKVSNKALPA 353
 DB 219 SGATFTWTPSSGK--SAVQGPPELDGCGYSVSVLPCCAQPMNHGETFTCTAAHPKLT 276
 QY 354 PIEKTIKAKGQPREPOVYITLPPSRREEMTKNQ-VSLTCLVKGYFSPDAVAVESWNGO--P 410
 DB 277 PUTANITKS-GNTFRPEVHLLPPSEALNELVTLTCLARGFSPKDVLRVLQSGQELP 335
 QY 411 ENNYKTTTPVLD-SDG--SFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQKSLSL 467
 DB 336 REKYLTVASRQEPSSQGTTFVAVTSILRVAEDWKKGDTFSCWGHGALPLATFQKTDRL 395
 QY 468 PGK 470
 DB 396 AGK 398
 RESULT 14
 Q9Y298 PRELIMINARY; PRT; 150 AA.
 ID Q9Y298
 AC Q9Y298
 DT 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE IGG VH PROTEIN PRECURSOR (FRAGMENT).
 OS IGG VH.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98322155; PubMed=9657749;
 RA Jacquemin M.G., Vander Elst L.P.L.;
 RT "Mechanism and kinetics of factor VIII inactivation: study with an
 RT IgG4 monoclonal antibody derived from a hemophilia A patient with
 RT inhibitor."
 RL Blood 92:496-506(1998).
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN
 DR EMBL; AJ224083; CAAL1829.1; -.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IgV; 1.
 KW Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT NON_TER 150 150
 SQ SEQUENCE 150 AA; 16031 MW; 563D164AB22802D5 CRC64;

Query Match 20.7%; Score 522; DB 4; Length 150;

Best Local Similarity 67.5%; Pred. No. 9.8e-35;
Matches 102; Conservative 15; Mismatches 30; Indels 4; Gaps 1;

Qy 1 MGWSCIILFLVATGTVHSGVQLVQSGAEVKKPGASVKVKSCASGYTFTSYMMQWVKQAP 60
| : : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : |||||
Db 1 MDWTWRILFLVAATGTHAQVQLVQSGAEVKKPGASVKVKSCGYTLTLPVHWGQAP 60
Qy 61 GQGLEWNGEIDPSDSTYNQKFKGKATLVDTSTAYMELSLRSEDATVYYCARNRD 120
| : : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : |||||
Db 61 GKLEWNGSFDPEGESIYAREFQGSVTMTADTSDIAYMELSLRSDDTAVYYCA---- 116
Qy 121 YSNWNWYFDVWGEGLTVTVSSASTKGPSVFPL 151
| : : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : |||||
Db 117 VPDPDAFDWCGGTMTVTVSSASTKGPSVFPL 147

RESULT 15
O95978 PRELIMINARY; PRT; 157 AA.
AC O95978;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE VHL PROTEIN PRECURSOR (FRAGMENT).
GN VHL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PERIPHERAL BLOOD;
RA Jox A., Zander T., Kuipers R., Irsch J., Kanzler H., Kornacker M.,
RA Bohlen H., Diehl V., Wolf J.;
RT "Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a
RT patient with mixed cellularly Hodgkin's disease is associated with
RT somatic mutations within the untranslated regions of rearranged and
RT class switch recombinated Ig genes.";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AJ005570; CAA06599.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Signal.
FT SIGNAL 1 21 POTENTIAL.
FT NON_TER 157 157
SQ SEQUENCE 157 AA; 17304 MW; 86986EDDA84D88B5 CRC64;

Query Match 20.1%; Score 505; DB 4; Length 157;
Best Local Similarity 62.4%; Pred. No. 2.5e-33;
Matches 98; Conservative 20; Mismatches 39; Indels 0; Gaps 0;

Qy 1 MGWSCIILFLVATGTVHSGVQLVQSGAEVKKPGASVKVKSCASGYTFTSYMMQWVKQAP 60
| : : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : |||||
Db 1 MDWTWRVFLAVAPGVHSGVQLVQSGAEIKRPGASVKVHCKTSGYVFTSYIIHWVRQPR 60
Qy 61 GQGLEWNGEIDPSDSTYNQKFKGKATLVDTSTAYMELSLRSEDATVYYCARNRD 120
| : : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : |||||
Db 61 GQGLEWNGGIGPGVGVSTWCAEKFQGLTMTNTSTTTVMELSLRLEFDTAVYFCGRGR 120
Qy 121 YSNWNWYFDVWGEGLTVTVSSASTKGPSVFPLAPSKS 157
| : : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : |||||
Db 121 WRSNGYNGHWGGTPTVTVSSSSTKGPSVFPLAPCSRS 157

Yu, Misook

To: STIC-Biotech/ChemLib
Subject: 09/499,662

Please search SEQ ID:107 and 117. Thanks.

Examiner Misook Yu, Ph.D.
703-308-2454 (Phone)
Art Unit 1642
CM1-8E18 (Room)
CM1-8E12 (Mail Box)

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Thu Apr 25 16:38:28 2002

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2002, 16:37:14 ; Search time 0.01 Seconds
(without alignments)
0.335 Million cell updates/sec

Title: us-09-499-662-1
Perfect score: 59
Sequence: 1 RTQNTKCRCK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 335 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : aaa63174.genpept.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	335	1	AAA63174

ALIGNMENTS

RESULT 1
AAA63174

Query Match 100.0%; Score 59; DB 1; Length 335;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10

Db 121 RTQNTKCRCK 130

→ 367

Search completed: April 25, 2002, 16:37:14
Job time: 0 sec

extracellular domain

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Schreiber, David

From: Yu, Misook
Sent: Wednesday, March 26, 2003 8:55 AM
To: Schreiber, David
Subject: 09/499,662

David, would you please do interferences search only for following proteins. All of them are small proteins. The case is due this biweek.

1. a single protein sequence: X(any 18-32 aa)-SEQ ID NO:2-X(any 14 aa)-SEQ ID NO:3-X(any 32 aa)-SEQ ID NO:4-X(any 11 aa).
2. a single protein sequence: X(any 23 aa)-SEQ ID NO:5-X(any 15 aa)-SEQ ID NO:6-X(any 32 aa)-SEQ ID NO:7-X(any 10 aa).
3. SEQ ID NOs: 50, 52, 54, 107, 109, 89, 117, 143, 145, 147, 157, 107, 127, 129, 131

Examiner Misook Yu, Ph.D.
703-308-2454 (Phone)
Art Unit 1642
CM1-8E18 (Room)
CM1-8E12 (Mail Box)

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09/499,662

Your SELECT statement is:

s hfe7a

Items File

8 5: Biosis Previews(R)_1969-2002/Apr W3
6 34: SciSearch(R) Cited Ref Sci_1990-2002/Apr W3
4 71: ELSEVIER BIOBASE_1994-2002/Apr W3
3 73: EMBASE_1974-2002/Apr W3
3 94: JICST-EPlus_1985-2002/Mar W2
2 144: Pascal_1973-2002/Apr W3
4 155: MEDLINE(R)_1966-2002/Apr W3
2 156: ToxFile_1966-2002/Feb W4
1 159: Cancerlit_1975-2002/Mar
1 172: EMBASE Alert_2002/Apr W3
7 399: CA SEARCH(R)_1967-2002/UD=13617

SYSTEM:OS - DIALOG OneSearch

File 5:Biosis Previews(R) 1969-2002/Apr W3

(c) 2002 BIOSIS

File 399:CA SEARCH(R) 1967-2002/UD=13617

(c) 2002 AMERICAN CHEMICAL SOCIETY

*File 399: Use is subject to the terms of your user/customer agreement.

RANK charge added; see HELP RATES 399.

File 34:SciSearch(R) Cited Ref Sci 1990-2002/Apr W3

(c) 2002 Inst for Sci Info

File 155:MEDLINE(R) 1966-2002/Apr W3

Set Items Description

S1 25 HFE7A

S2 12 RD (unique items)

136052721 CA: 136(4)52721g PATENT

The medicine which contains the human conversion anti- Fas antibody.

INVENTOR(AUTHOR): Serizawa, Nobuki; Haruyama, Hideyuki; Nakahara, Kaori;

Tamaki, Ikuko

LOCATION: Japan,

ASSIGNEE: Sankyo Co., Ltd.

PATENT: Japan Kokai Tokkyo Koho ; JP 2001342148 A2 DATE: 20011211

APPLICATION: JP 200193106 (20010328) *JP 200090918 (20000329)

PAGES: 194 pp. CODEN: JKXXAF LANGUAGE: Japanese CLASS: A61K-039/395A;

A61K-038/00B; A61P-001/16B; A61P-007/06B; A61P-009/00B; A61P-009/10B;

A61P-013/12B; A61P-019/02B; A61P-029/00B; A61P-037/00B; A61P-037/06B;

Set Items Description

S1 25 HFE7A

S2 12 RD (unique items)

S3 3682 ANTI(W)FAS

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09/499, 662

2/9/6

DIALOG(R) File 155:MEDLINE(R)

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13268098 21926856 PMID: 11929798

Murine acute graft-versus-host disease can be prevented by depletion of alloreactive T lymphocytes using activation-induced cell death.

Hartwig Udo F; Robbers Michael; Wickenhauser Claudia; Huber Christoph
Division of Hematology, III Department of Medicine, University Medical
School Mainz, Germany. uhartwig@mail.uni-mainz.de

Blood (United States) Apr 15 2002, 99 (8) p3041-9, ISSN 0006-4971

Journal Code: 7603509

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: AIM; INDEX MEDICUS

Depletion of T lymphocytes from allogeneic bone marrow transplants successfully prevents the development of graft-versus-host disease (GvHD) but is associated with impaired engraftment, immunosuppression, and abrogation of the graft-versus-leukemia effect. We therefore explored the possibility of selectively eliminating alloreactive T cells by CD95/CD95L-mediated activation-induced cell death (AICD) in a major histocompatibility complex allogeneic murine model system. Activation of resting or preactivated T lymphocytes from C3H / HeJ (H-2(k)) mice was induced with irradiated BALB/cJ (H-2(d)) mouse-derived stimulators. Substantial decrease (> or = 80%) of proliferative and lytic responses by activated alloreactive T cells was subsequently achieved by incubating the mixed lymphocyte culture with an agonistic monoclonal antibody to CD95, and residual T cells recovered did not elicit alloreactivity upon challenge to H-2(d). Depletion of alloreactive T lymphocytes by AICD was specific because reactivity to an I-A(d)-restricted ovalbumin (OVA) peptide by OVA-specific CD4(+) T cells mixed into the allogeneic T - cell pool and subjected to induction of AICD in the absence of OVA peptide could be preserved. Adoptive transfer of donor-derived allogeneic T lymphocytes, depleted from alloreactive T cells by AICD in vitro, in the parent (C3H/He) to F(1) (C3H/He x BALB/c) GvHD model prevented lethal GvHD. The results presented suggest that alloreactive T cells can effectively be depleted from allogeneic T cells by induction of AICD to prevent GvHD and might introduce a new strategy for the separation of GvH-reactive T cells and T cells mediating antiviral and possibly graft-versus-leukemia effects.

Set	Items	Description
S1	2554	C3H(W)HEJ
S2	384	S1 AND T(W)CELL?

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2/9/3 (Item 3 from file: 5)
DIALOG(R) File 5: Biosis Previews(R)
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09623755 BIOSIS NO.: 199598078673

Regulation of apoptosis and T cell activation by Fas -specific mAb.

AUTHOR: Alderson Mark R; Tough Teresa W; Braddy Steven; Davis-Smith Terri;
Roux Eileen; Schooley Ken; Miller Robert E; Lynch David H(a)

AUTHOR ADDRESS: (a)Dep. Immunobiol., Immunex Res. Dev. Corp., Seattle, WA
98101**USA

JOURNAL: International Immunology 6 (11):p1799-1806 1994

ISSN: 0953-8178

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: **Fas** was initially described as a molecule expressed on the surface of certain cell lines that could mediate programmed cell death (apoptosis) subsequent to ligation by specific mAb. To determine whether mAb to other epitopes on the **Fas** molecule might mediate other functions, we generated a panel of mAb to the extracellular portion of human **Fas**. Significant lysis of **Fas**-expressing target cells was only observed when the new mAb were first bound to a solid-phase support and not when the mAb were added in solution. However, several of these mAb inhibited the killing of target cells induced by the prototypic **Fas**-specific mAb, CH-11. Those mAb that inhibited apoptosis of target cells mediated by the **CH - 11 mAb** also blocked lysis of target cells mediated by cells expressing **Fas** ligand. Finally, some of the **Fas**-specific mAb were found to co-stimulate proliferation of peripheral blood T cells in the presence of immobilized CD3 mAb. Thus, the data indicate the existence of a complex set of interactions mediated by **Fas** in both normal and transformed lymphoid cells that may have important implications regarding the role(s) of this molecule in regulation of immune responses.

Set	Items	Description
S1	12	CH(W)11(W)MAB AND FAS
S2	4	RD (unique items)

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09/499,662

WEST Search History

DATE: Friday, August 30, 2002

Set Name Query

side by side

Hit Count Set Name

result set

DB=USPT; PLUR=YES; OP=OR

L22	L9 and "ferm bp"	0	L22
L21	L9 and "Ferm bp-5828"	0	L21
L20	L14 and ferm	4	L20
L19	L15 and frem bp	42949	L19
L18	L14 and hfe7a	0	L18
L17	L11	0	L17
L16	L12 and cd-95	0	L16
L15	L11 and epitopes	0	L15
L14	L10 and conserved	88	L14
L13	(L1 and "ferm bp") AnD (((@pd > 20020425)!))	0	L13
L12	(L1 and "Ferm bp-5828") AnD (((@pd > 20020425)!))	0	L12
L11	L9 and extracellular	0	L11
L10	anti-fas	166	L10
L9	(L6 and ferm) AnD (((@pd > 20020425)!))	0	L9
L8	(L7 and frem bp) AnD (((@pd > 20020425)!))	1709	L8
L7	(L6 and hfe7a) AnD (((@pd > 20020425)!))	0	L7
L6	(L3) AnD (((@pd > 20020425)!))	5	L6
L5	(L4 and cd-95) AnD (((@pd > 20020425)!))	2	L5
L4	(L3 and epitopes) AnD (((@pd > 20020425)!))	4	L4
L3	(L2 and conserved) AnD (((@pd > 20020425)!))	5	L3
L2	(L1 and extracellular) AnD (((@pd > 20020425)!))	6	L2
L1	(anti-fas) AnD (((@pd > 20020425)!))	12	L1

END OF SEARCH HISTORY

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